Example 1; SEQ ID NO 19298; 1481pp; English.

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the treatment, prevention and diagnosis of medical conditions caused by Pacnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes vilgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used a diagnostic agents for determining P. acnes proteins may also be used as diagnostic agents for determining P. acnes presence, for example, by this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 KGELAMRNIEARGLKOMKRQGDANVKGE-EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH 126
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Jones R, Carter D;
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Benson DR,
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Lodes MJ,
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Barth B, Vallieve-Douglass J;
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Zhang Y, Wang S, Jen S
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The invention relates to an isolated polymucleotide (Archests). Acres 47.33) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasse expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide for stimulating an immune response specific for a P. acnes polypeptides of the invention; a method for stimulating an immune response specific for a P. acnes polypeptides, and a mithodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the development of P. acnes in a parient; and a method for inhibiting the development of P. acnes in a parient; and a method for inhibiting the development of P. acnes in correcting. The P. acnes polypeptides, polymucleotides, attibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for adaposing, preventing or treating acne correcting. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes polymucleotides can also be used as probes or primers for a sequence represents a polypeptide prame) contained within the P. acnes polymucleotides of the canding trame) contained within the P. acnes polymucleotides of the canding frame) contained within the P. acnes polymucleotides of the cinvention. Note: The sequence data for this patent did not form the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequence.
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                                                                         The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 PGSPAPANFLDIGGGASAEIMANGLDLIMSDEQVRSV--FVVVVFGGITACDOV 372
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    S. epidermidis open reading frame protein sequence SEQ ID NO:50.

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Best Local Similarity
Matches 45; Conserva:
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
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                   WPI; 2001-316495/33.
N-PSDB; AAH52328.
                                                                                                                                                                     Sequence 817 AA;
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         Kimmerly WJ;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts calls which express the colypeptides. The polypeptides (II) (and/or nucleic acids) may then be polypeptides my also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the colympostides my also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the control of S. epidermidis infections, e.g. endocarditis AAH53971 to treatment of S. epidermidis infections, e.g. endocarditis AAH53971 to compound the present invention DNA AAH5509 represent specifically claims from the present invention of the present invention in the present invention of the present invention in the compound only the present invention in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present in the control of the present present though sequences are present in the control of the present and primers are present in the control of the present and primers are present in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                        c acids encoding polypeptides from Staphylococcus epidermidis, for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 432; 2188pp; English.
                                                            09-NOV-2000; 2000WO-US030782
                                                                                                                             99US-0164258P
                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                    WPI; 2001-316495/33.
N-PSDB; AAH53067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 817 AA;
                                                                                                                             199-NOV-1999;
                                                                                                                                                                                                                                                          Kimmerly WJ;
17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                      AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and lave antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. c. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, eg. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA copyneare sequences from the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences and primers which are used in the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | ::: | | ::: | | ::: | K-----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTVIIMTSNVGAQ 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 DILHKRVIGQNDAVNSİSKAVRRARAĞLK----DP-----KRPIĞSFIFLĞPTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 VGKTELARALAESMFGEDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 45; Gaps
                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 ELODORFAGFGGASEGSDYETVRKTMMKELKNSFRPE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 84.5; Di
Best Local Similarity 23.0%; Pred. No. 11;
Matches 50; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 59; 2188pp; English
          (GLAX ) GLAXO GROUP LTD
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549 VGXTELARALAESMFGEDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                                                                                                                                                             121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                 609 K----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTVIMTSNVGAQ 663
                                                                                73 MRNIE-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY
                                                             DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
    DB 4; Length 817;
                                  Indels
                                                                                                                                                                                                                                        SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                            ELODORFAGEGGASEGSDYETVRKTMMKELKNSFRPE 700
                                  87;
      7.9%; Score 84.5; Di
23.0%; Pred. No. 11;
Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                                            ABU43148 standard; protein; 817 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
19-JUN-2003
                                                                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                        ABU43148;
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Protein encoded by Prokaryotic essential gene #28675.

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the invention tradeces given in the call couplibring any one of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated propagated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway considered for proliferation, or that inhibits proliferation or the biological identifying a gene product or that has an activity against a biological pathway in which a proliferation required for cellular proliferation of an identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene or organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene or to which each of the strains is present in a culture or collection of the strains or strains; or (3) identifying the target of a compound that inhibits the culture or collection of conditional proteins or screening for homologus nucleic acids are useful for an dentifying proteins or screening for homologus mucleic acids required for cellular promerance or proliferation of an organism. The antisense candidate are useful for cellular provery processed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : | : | : | | | DTLHTRVIGQNDAVNSISTAVRARAGLK----DP------KRPIGSFIFLGPTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPIH----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
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                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 71072; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
                                                                                                                                                                                                                                        06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-034293P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                         Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                              ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029926/
N-PSDB; ACA47018/
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                                                                         WO200277183-A2
                                                                                                                                                                                                                 21-MAR-2001;
                                                                                                                      03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
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Matches
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to sorteen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
549 VGKTELARALAESMFGEDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                                     609 K----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTVIIMTSNVGAO 663
                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 DILHKRVIGONDAVNSISKAVRRARAGLK-----DP-----KRPIGSFIFLGPTG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 DPIH----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                              121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4081,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Indels
                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%; Score 84.5; D
23.0%; Pred. No. 11;
Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4081; 267pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                   ABP39236 standard; protein; 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-00134001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0055779P.
97US-0064964P.
                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABN91781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 823 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        JS6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2002.
                                                                                                                                                                                                                                                                                     24-JUL-2002
                                                                                                                                                                                                                                                     ABP39236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                 RESULT 64
ABP39236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABB130511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
1256 IBIIVRQMLQKVRITDPGDTTLLFGEDVDKKEFYEENRRTEEDGGKPAQAVPVLLGITKA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806 DYGPESRGFVENSY----LAGLTPSEFYFHANGG-REGLIDTAVKTAETGYIQRRLIKA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 D-----IVSMEYDLAYKLGDLHPTT---HVISDIQDFVVALSLEISDEGNI-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHA--DKFERHVGIV-----DFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GDANVKGEE---GIVKAHLLIGVHD
                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO 1527; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.5; DB Pred. No. 36; 33; Mismatches
                                                          1316 SLGTESFISAASFODT----TRVLTDA 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EW;
                              178 IFGVLSDVLTALFQDTVRKEMTKVLAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ELAMRNI-EARGLKOMKRO------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers
                                                                                                                                 ABB58245 standard; protein; 1887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.9%; Sco. 22.7%; Precitive 33; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li
                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1887 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                     WO200171042-A2.
                                                                                                                                                                                                                                                              pharmaceutical
                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                               Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
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                                                                                                                                                              ABB58245
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Matches
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                                                          임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LSILDP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genttal diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, operinepathits, bartholhinitis, penumopathy in breast feeding infants; and veneraal lymphogramulomatosis. The polypeptides of the invention may be of use in treating these diseases
      ------MKRQ 87
                                                                                                                                                                                                                                                             Vaccine, eye disease, conventional trachoma, nonendemic trachoma, paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, bartholinitis, pneumopathy, venereal lymphogranulomatosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1396;
                                                                                                                                                                                                                                     Protein involved in intermediate metabolism of polypeptides.
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                                                 173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                            670 ELODORFAGFGGASEGSDYETVRKTMMKELKNSFRPE 706
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Pred. No. 23;
94; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 739-741; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of Chlamydia trachomatis.
                                                                                                                                                   Ä.
                                                                                                                                                     standard; protein; 1396
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23.6%; Pre
tive 34;
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97FR-00016034.
98US-0107077P.
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les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1396 AA;
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17-DEC-1997;
04-NOV-1998;
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                         615
                                                                                                                                                                                AAY36871;
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                                                                                                                        RESULT 65
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12;

Gaps

79;

745 109 805 153

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DPIHYDKITEEINKAI-DDAIAAIEQSETIDPMKVPDHADKFERHVGI-VDFKGELAMRN

18

204 LSKDKIKQEVKE-----SYERLLKDSPQAG-----VEVSYDSNYLLGFLINTLADSOTT

ROLLSDMSQATVGMPFSQFHEGH 275 129 THVISDIQDFVVALSLEISDEGN 151

IEARGIKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLG-----DLHPT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
       184
                                            860 MEŠVMVNYDGTVRNSVĠQLIQLRYGEDGLCĠELVEFQNMPTVKLSNKSFEKRFKFDWSNE 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infecdisease caused by Streptococcus bacteria, such as meningitis, and detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relford J, Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus polypeptide SEQ ID NO 3268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3480-3481; 4525pp; English.
                                                                                                                                                                                                                                                                    ABP27046 standard; protein; 306 AA.
MISFEVROFANVVNHIGGLSIL-
                                                                                                -VLTAIFQDTVRKEMT 199
                                                                                                                               27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-352536/38.
N-PSDB; ABN67677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H;
                                                                                                185
                                                                                                                                                                                                                                                                                                                     ABP27046;
                                                                                                                                                                                                                  RESULT 67
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 MRNIEARGLKQMKRQGDANVKGEEGIVKAH----LLIGVHDDIVSME--YDLAYKLGDL- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AVSADPIHYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                      Antibacterial; vaccine; gene therapy; infection; sepsie; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 84; DB 6; Length 397;
larity 24.1%; Pred. No. 4.4;
Conservative 35; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2726; 49pp; English.
                                                                                                                                                                              Staphylococcus aureus protein #1363.
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ABM72123 standard; protein; 397 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001; 2001GB-00007661.
                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
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N-PSDB; ACF73683.
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Local Sim.
45;
                                                                                                                   20-NOV-2003
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                                                           ABM72123;
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Matches
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This invention describes novel human nucleic acid (CDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAYS941-Y60328 represent protein fragments encoded by the human endometrium tumour cDNA library derived EST fragments represented in AAZ41981-Z42121
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                                                                                                               | :: | | :: | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
130 VANKPASGTQIIDEWGEHQMKTGDLIVYTSADPVLQIAAHEDIIPLEELYDICEKVRELT 189
                                                                        HPTTHVISDIODFVVALSLEISDEGNITMIS----FEVROFA-NVVNHI--GGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endometrium, human, tumour, cancer, anticancer, cytostatic, EST: treatment, uterine, gene therapy, expressed sequence tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded protein 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived polypeptides, for treatment or identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY59996 standard; protein; 410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 297; 444pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98DE-01017948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endometrium tumour EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 22.13
Matches 40; Conservative
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                                                                                                                                                                                                                          179 FGVLSDV 185
                                                                                                                                                                                                                                                                            | ::|:
243 IGKINDI 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE19817948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-1999,
                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59996
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 69
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The present invention is related to a Lactococcus lactis mucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-07T-2001) which is available in electronic format directly from WIPO at the business of the production of standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454
                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|::||| :::
397 YEKVSSEINHLLEEGFRVLVLAGTKE--KIYDQLNLGAYALGYVVLANPIRENAKSTFNY
                 355 DQFGFINYEVGDSKKLFFHVKEVQD---GIBLQAGDE-----VEFSVIPKSSGGL
                                                       ----YKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                            Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 YDKITERINKAIDDAIAAIRQSETIDPMKVPDHADKFERHVGIVDFKGEL---
LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 775;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Renault P, Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ς.
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Pred. No. 11;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 587; 2504pp; French.
                                                                                                                                                                                                                            ABB53885 standard; protein; 775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%; Scor
19.8%; Pred
ative 37; 1
                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis protein yfgQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-00004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 IEARGLKOMKROGD----
                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 775 AA;
                                                                                                                      173 S 173
                                                                                                                                                    402 A 402
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16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotine A,
                                                                                                                                                                                                                                                          ABB53885;
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VSADPIHYDXITEEINKAIDDAIAAIEQSETIDPMKVPDHAD-KFERHVGIV---DFKGE 70

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KFLLIAAVAFVAVSADPIHYD----KIT--EEINK--

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The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polyene antibiotic amphotericin responsible for the biosynthesis of the polyene antibiotic amphotericin setul for preparing amphotericin derivatives or analogue antibiotic amphotericins with altered properties and in the biosynthesis of polykeides other than amphotericin ampholil, ampholil or ampholi mutants are useful for producing amphotericin derivatives glycosylated with alternative cugars, ampholil or ampholi or ampholi or ampholi or ampholi or ampholi amphotericin-lambic cronside B; ampholil or ampholi ampholic ampholic ampholic ampholic ampholic ampholic ampholic ampholic or ampholi  or ampholic and ampholic and ampholic and ampholic and ampholic and ampholic and ampholic or an originate of the preparing polypeptides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine. The present sequence is polyketide synthase multienzyme housing extension modules 9, 10, 11, 12, 13 and 14 encoded by 8. nodosus amphil gene
                                       ---IGVHDDIVSMEYD----LAYKLGDLHPTTHVISDIQDFVVALSLEISDE 149
                                                                                                                       GNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTK-----V 201
                                                                                                                                                 FAEQGVNIKVISGDNPQTVSAVAKRAGITGAERFIDANLLKTKEDLDQAVESYTVFGRVT 514
                                                                              PDOKRRIVQALKRKÖHTVAMTGÖGVNDILAMKSAÖCSIAMASGSDAATQVAQVVLLDSÖF 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, useful for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyene; antibiotic; amphotericin; amph; polyketide synthase; enzyme.
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7.9%; Score 84; DB 6; Length 9510;
Best Local Similarity 24.5%; Pred. No. 4e+02;
Matches 53; Conservative 39; Mismatches 80; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces nodosus amphI gene encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 120-162; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                AAE36119 standard; protein; 9510 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-2002; 2002WO-IE000071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001; 2001IE-00000527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV COLLEGE DUBLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                            635 GIPGFLLSLEN 646
                                                                                                                                                                                                       LAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces nodosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-201271/19.
N-PSDB; AAD54645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200297082-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amphotericin
                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2003
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  155
                                                                                515
                                                                                                                       150
                                                                                                                                                                                                       202
                                         105
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                                                                                                                                                                                                                                                                                                           RESULT
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium bacteria are useful for producing amino acids, nucleic acids, vitemins, saccharides and organic acids, particularly 1-1ysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                               45 TIDPMKVPDHA--DKFERHVGIVDFKGELAMRNIEARG-LKQMKRQGDANVKGEEGIVKA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                        642 EVKPDHLAGHSVGEIAAAHVAGV-FSLDDAATLVAARGRLMQALPEGGAMVAVQASEDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ochiai K, Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium, amino acid synthesis, vitamin, saccharide, organic acid synthesis.
                                                                                                        102 HLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDPVVALSLEISDEGNIT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; SEQ ID NO 3526; 246pp + Sequence Listing; English
                                                                                                                                                                           185
                                                                                                                                                                                             H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                          protein fragment SEQ ID NO: 3526.
                                                                                                                                                                         154 ----MISFEVROFANVVNHIGGLSILDPIFGVLSDV
                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                        AAG89772 standard; protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-00127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizoguchi B
Senoh A,
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                                                                                                                                                                                                                                                                                                                                                                                           glutamicum
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Tateishi N
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Length 412;

DB 4;

Score 83.5;

7.88;

Query Match

10;

Gaps

44;

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to mucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an enthodo of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the polynucleotide and/or activity of the polynucleotide and/or polypeptide; and for conting sequences corresponding to the cDNA sequences of the invention (ADC32627) and the polypeptides encoded by the contigs (ADC32628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                      54 HADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                       Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; uno disease; cancer; encer marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                         ---- QWEEGSARPVAALGVSDN-VS
                   17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weng G;
                                                                                                                               114 MEYDLAYKLGDLHPTTHVISDI-----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                184 YTYDINRPIGD-RVTSVTIDDTPLDPERDYVVAASLYL-QSGNEGMTA 229
                 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                     Human novel polypeptide sequence, SEQ ID NO:1069.
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Asundi V,
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; SEQ ID NO 1069; 1185pp; English.
31.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY, Zhang J, Ren F, Xue AJ,
P, Ghosh M, Wang D, Ma Y, A
y-Vicente D, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; chromosome 15q21.3
                                                                                                                                                                                                                                                          ADC30987 standard; protein; 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2001; 2001US-0324631P.
                     Conservative
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 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADC30016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003029271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                    18-DEC-2003
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                     34;
                                                                                                                                                                                                                                                                                               ADC30987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer.
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                     Matches
                                                                                                                                                                                                                       RESULT 73
                                                                                                                                                                                                                                          ADC30987
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                                                                                                                                                                                                                  disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 HIGKTIEKLQKEMADIVEASRTSTLELQNQLDEYKEKNRRE--LAEMQRQLKEKTLEABK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 -GLKQMKRQGDANVKGE------EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ADC33394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 517;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #36108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 83.5; DE 21.7%; Pred. No. 7.3; ive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRLVKQMEDKVSQLEMELEEERN 297
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Carr GJ,
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2001US-0342923P.
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Best Local Similarity 21.73
Matches 31, Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 517 AA;
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Wall D,
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide, or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway to proliferation or that has an activity against a biological pathway in which a proliferation or the test compound that inhibits expoliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for required gene or its gene product lies organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for underexpressed, it (10) profiling the expect proliferation of an organism; or (13) identifying the target of a compound that inhibits the compound, sactivity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits and discovery programs, or for screening honologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, X. preumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY----- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
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                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 RQFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VAVSADPIHYDKITEEINKAIDDA-IAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
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                                                Claim 25; SEQ ID NO 78505; 1766pp; English.
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les 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequences of the invention are useful for the diagnosis and protein sequences of the invention are useful for the diagnosis and protein sequences of the invention are useful for the diagnosis and recament of: arteriosclerosis, arteriosclerosis, orintosis, heaptitis, whellow fever, influenza, measles, mumps, HIV, human T lymphotropic virus, rabies, gastroenteritis, encephalitis, rubella, espleopy, ischemenic cerebrovascular disease, stroke, cerebral neoplasm, Alzhaimer's disease, pick's disease, Huntington's disease, dementia, Parkinson's disease, schools, meaningitis, brain abscess, prion disease, creuzfeldt-Jakob disease, insomnia, neurofibromatosis, cerebral palsy, myasthenia gravis, anxiety. The present amino acid sequence represents a human SCAP of the
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ischaemic cerebrovascular disease; stroke; cerebral neoplasm; Alzheimer's disease; Pick's disease; Huntington's disease; dementia; Parkinson's disease; amyotrophic lateral sclerosis; atrophy, hereditary ataxia; multiple sclerosis; meningitis; brain abscess; prion disease; Creutzfeldt-Jakob disease; insomnia; neurofibromatosis; cerebral palsy; myasthenia gravis; anxiety.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richardson IW, Tang YT, Thangavelu K;
). Chawla NK, Hafalla AJA, Swarnakar A;
E, Baughn MK, Lu DAM, Arvizu CS, Kable AE
Jiang X, Jackson AA, Khare R, Elliott VS;
e S, Lehr-Mason PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polypeptides useful for treating e.g. celidisorders, viral infections and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%; Score 83.5; D
21.7%; Pred. No. 13;
ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 THVISDIQDFVVALSLEISDEGN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue H, Griffin JA, Richardson TW, Forsythe IJ, Becha SD, Chawla NK, Marquis JP, Gorvad AE, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRLVKQMEDKVSQLEMELEEERN
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2002US-0381599P.
2002US-0387270P.
2002US-0397125P.
                                                                                                                                                                                                                                                                                                    2002US-0351715P.
                                                                                                                                                                                                                                              16-JAN-2003; 2003WO-US001772
                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramkumar J, Jiang
A, Xu Y, Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.77
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-671468/63.
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                                                                                                                                                                      WO2003062391-A2
                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2002;
                                                                                                                                                                                                                                                                                                                        .5-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                           17-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee SY, Ram
Bulloch SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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164 TQMLFAHHGLTLRDKK--APSVFFVKKLKNTLNHVYGYAVL----SISSKQLANLFQSVV 217
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05-MAY-2000; 2000US-00565501.
14-AUG-2000; 2000US-00639206.
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                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto A,
                                                 RKEMTKV 201
                                                                                           218 NPEISKI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probst P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-061971/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS96071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179276-A2.
                                                                                                                                                                                                                                                                                                         26-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed SG, (
Coler RM,
                                                 195
                                                                                                                                                                                                                                                          AAU71861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid derived from Enterococcus factium encoding an Enterococcus factium polypeptide having none of 10 fully defined sequences given in the (or comprising 40 sequential nuclectides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acids is useful for diagnosing pathological conditions infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection, and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans nucleic acid is useful for recombinant production of Candida albicans and vaccines conteaining the nucleic acid are useful for preventing or treating Enterococcus faccium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ESLNDTIENTLAAFDSNPAVKSYFSNDPAQHME------QLQQQLRTIQK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 MNDSLSKIHPMIDYDVLIFGENG----RTFVG-NDMLTAVSADSFFQSAIAQRVNERAAD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 QGDANVK-------GEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISD 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Gaps
                                                                                                                                                                                                                              Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 83; DB 7; Length 583;
18.7%; Pred. No. 9.8;
tive 36; Mismatches 76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 5678; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating Enterococcus faecium infections.
one if the disclosed E. faecium proteins.
                                                                                                                                                                                         E. faecium protein sequence SEQ ID 5678.
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                                               ADC96051 standard, protein; 583
                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00107532.
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98US-0085598P.
                                                                                                                                          (first entry)
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Best Local Similarity 18.7
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bush
                                                                                                                                                                                                                                                                                                         Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                     US6583275-B1
                                                                                                                                          01-JAN-2004
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                                                                                              ADC96051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Leishmania antigens, useful for prevention, treatment and diagnosis of leishmaniasis, also related nucleic acids for genetic
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17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania antigen 4G2-83 extended protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 83; 23.3%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Webb JR,
AAU71861 standard; protein; 845 AA.
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10;

Gaps

34;

70;

34; Mismatches

Conservative

42;

88 52 144

53 DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100

83

145 EISDEGNITMTSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP

2 VNFTVDQVRELMDYPDQIRNMSVIAHVD------HGKSTLSDSLVGAAGIIXMEEAG DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL

29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG

204

Mon

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide containing an immunogenic portion of a Leishmania antigen or its variant which has antiparasitic and immunostimulant activity. The compositions and methods of the present invention are useful for preventing, treating and detecting invention are useful for preventing, treating and detecting leishmaniasis, and stimulating immune responses in patients against leishmaniasis. The polypeptides and the polymucleotides encoding them can be used for gene therapy, in vaccines or as interleukin-12 agonists. The compositions and methods of the present invention, as compared to prior art, are more improved therapeutic modalities in the diagnosis,
              Dillon DC, Skeiky YAW, Bhatia A;
EISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                                                                                                                                                                                       Antigen; immunogenic; antiparasitic; immunostimulant; leishmaniasis; gene therapy; vaccine; interleukin-12 agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide containing at least an immunogenic portion of
Leishmania antigens or their variants, useful for preventing,
and detecting leishmaniasis, and stimulating immune responses
                                                                                                                                                               L. major 4G2-83 extended antigen SEQ ID 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 108-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Webb JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto A, Webb Ji
Probst P, Brannon M;
                                                                                     AAB71315 standard; protein; 845
                                                                                                                                                                                                                                                                                                                            22-SEP-1995; 95US-00531669.
12-FEB-1997; 97US-00798841.
12-FEB-1998; 97US-00022765.
30-GCT-1998; 98US-00183861.
14-APR-2000; 2000US-00551974.
65-MAX-2000; 2000US-0055501.
                                                                                                                                                                                                                                                                                                      2001US-00874923
                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           REED S G.
CAMPOS-NETO A.
WEBB J R.
DILLON D C.
SKEIKY Y A W.
                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLER R N.
PROBST P.
BRANNON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-635457/68
                                                                                                                                                                                                                            Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BHATIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF88573
                                                                                                                                                                                                                                                     US2002081320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 845 AA;
                                                                                                                                                                                                                                                                                                     04-JUN-2001;
                                                                                                                                     18-NOV-2002
                                                                                                                                                                                                                                                                              27-JUN-2002
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                                                                                                             AAB71315,
                         101
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(PROB/)
(BRAN/)
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(SKEI/)
(BHAT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (REED/)
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(WEBB/)
                                                             RESULT
AAB7131
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Length 845;

Score 83; DB 5; Pred. No. 17;

7.8%;

Query Match Best Local Similarity

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The invention relates to an isolated polypeptide comprising an immunogenic portion of a Leishmania antigen or its. Also included are antigenic epitopes, fusion proteins comprising an isolated polypeptide fusion protein comprising at least two contiguous antigenic epitopes, polynucleotides encoding the antigens or fusion proteins, a recombinant expression vector comprising the polynucleotide, a host cell transformed with the vector and a composition (pharmaceutical or immunogenic) comprising the antigen or fusion protein and a physiologically acceptable carrier. The compositions are useful for inducing protective immunity
                       151
                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen, protozoacide, antibacterial, virucide, cytostatic, immunostimulant, leishmaniasis, Leishmania infection, immune response, interleukin-2 stimulation, cancer, bacterial infection, viral infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polypeptide useful for preventing or treating leishmaniasis, comprises an immunogenic portion of a Leishmania antigen
101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL-----RQALTERIRP
                                                                                                                                                                                                                                                                                                                                                                     Leishmania T cell antigen 4G2-83 extended protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dillon DC;
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                                                                                                                                                                                 ADB78873 standard; protein; 845 AA.
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97US-00798841.
97US-00920609.
98US-00022765.
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2000US-00565501
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04-JUN-2001; 2001US-00874923
                                                                                                                                                                                                                                                                                                            (first entry)
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CAMPOS-NETO A.
WEBB J R.
DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-605673/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protozoan infection
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30-OCT-1998;
14-APR-2000;
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14-AUG-2000;
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12-FEB-1997;
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(WEBB/)
(DILL/)
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                                                                                                                 RESULT 7
ADB78873
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against leishmaniasis in a patient. The fusion protein is useful for the detecting Leishmania infection in a patient by contacting dermal calls of the patient with the composition and detecting an immune response on the patient's skin, where the immune response is induration. The compositions are useful for stimulating a cellular and/or humoral immune response in a patient, or for treating a cellular and/or humoral immune response in a interleukin (IL)-2 stimulation, where the disease responsive to interleukin (IL) as bacterial, viral or profozoan infection. The antigen is useful for preventing or treating leishmaniasis. The present sequence represents a Leishmania antigen (or fragment).
                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DANY----KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL
                                                                                                                                                                                                                                                                                                                                                                                 29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKROG
                                                                                                                                                                                                                                                                                                                                                                                                                EISDEGNITMISFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                                                                                                                                                                                                                                                                                                                                         34; Gaps
                                                                                                                                                                                                                                                                                          Length 845;
                                                                                                                                                                                                                                                                                                                                       70; Indels
                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                             7.8%; Score 83; DB 23.3%; Pred. No. 17; ative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                       42; Conservative
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     Seguence 845 AA;
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ABB53805 standard; protein; 1060 AA
                                                                                               (first entry)
                                                                                 (revised)
                                                                                29-AUG-2003
                                                                                             16-MAY-2002
                                                     ABB53805;
             ABB53805
RESULT
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Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese. Lactococcus lactis protein dnaE. 11-APR-2000; 2000FR-00004630. Lactococcus lactis; IL1403 FR2807446-A1 12-OCT-2001

(INRG) INRA INST NAT RECH AGRONOMIQUE

11-APR-2000; 2000FR-00004630.

Ehrlich SD; Renault P, Sorokine A, Bolotine A,

WPI; 2002-043418/06.

New nucleotide sequence useful in the identification or Lactococcus lactis and related species. Claim 6; SEQ ID NO 507; 2504pp; French.

The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in

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                                                                                                                                                                91 NVKGE----EGIVKAHLLIGVHDDIVSMEYDLAYK-----LGDLHPTTHVISDIQDF-- 138
                                                                                                                                                                                                                                                              59 OPIISIELNFEWRGLPIAFSFIAKDTEGYKNLLRISTLHNYGRROFSDIONHLSGIALII 118
                                                                                                                                                                                                                               -----NI----TMTSFEVROFANVVNHIGGLSILD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The GroEL heat shock protein (AAW16678) of Lawsonia intracellularis can diseases, esp. to protect birds and animals against intestinal diseases, esp. to protect pigs against porcine proliferative enteropathy. It is the expression product of a DNA molecule (AAT69201) obtd. by screening an L. intracellularis library with rabbit anti-1. intracellularis sera. GroEE, GAV816680-85) can do ther. L. intracellularis polypeptides (AAW16680-85) can be administered as recombinant polypeptides or expressed as recombinant vaccines utilising polypeptides or viral vectors. Antibodies raised against the polypeptides may be useful in immunotherapy, diagnosis of infection and detection
                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intestinal disease; porcine proliferative enteropathy; vaccine; GroEL; immunotherapy; antibody; diagnosis; heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine for treating or preventing Lawsonia intracellularis infection especially in pigs, containing non-pathogenic form of bacterium or its
                                                                                                                                                                                      6 NIKTEYSFLDSVVKV-----DDYLETAHRLGYQTVGICDVGNLHAAFRFVRKAQKFNL
electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                    Gaps
                                                                                                                                    52;
                                                                                                  Length 1060;
                                                                                                                                    Indels
                                                                                                                                    38;
                                                                                                     5;
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                                                                                                                                                                                                                                                                                                 P-IFGVLSDVLTAIFQDTVRKEMTKVLAPAF 206
                                                                                                   7.8%; Score 83; DB: 21.2%; Pred. No. 23; ive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               AAW16678 standard; protein; 548 AA
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95AU-00006911.
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(PIGR-) PIG RES & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                     Query Match 7.8
Best Local Similarity 21.2
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawsonia intracellularis
                                                                                                                                                                                                                                   139 -- WALSLEISDEG-
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N-PSDB; AAT69201.
                                                                      Sequence 1060 AA;
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                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW16678;
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Best Local Similarity
Matches 39; Conserv
  N-PSDB; ABX34508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 953 AA;
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                                                                                                                    or hepatitis.
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                                                                                                                                                                                      VKLVAAGRNPM-----AIKRGIDKAVVAV--TKELSDITKPTRDQKEIAQVGTISANS 154
                                                                                                                                                                                                                                      ELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY----- 120
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                                                                                                                                                                                                                                                                                                                                    -----KLGDLHPTTHVISDIQDFVVALSLBISDEGNITMTSFEVR 160
                                                                                                                                                                                                                                                                                                                                                                209 EKMYCELDNPYILCNEKKITSMKDMLPILEQVAKVNRPLLIIAEDVEGEALATL----- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEÄIFEDRGIKLENVSLSSLG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; seteopathic; cytosfatic; anti-INV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cencer; adehocarcinoma; leukaemia; lymphoma; melanoma; mysloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; AIDS;
                                                                                                                                           10 VAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKG 69
                                                                                                                                                                                                                                                                                                                                                                                                                             161 QFANVVNHIGG----LSILDPIFG----VLSD--VLT---AIFQD------
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, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Rleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urasaka ME;
                                                                                           87;
                                                Length 548;
                                                                                           83; Indels
                                                2;
                                                DB
                                             ; Score 82.5; D; Pred. No. 10; 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAKRVVIDKENTTIVDGAGKSE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TVRKEMTKVLAPAFKRE 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MDDT polypeptide SEQ ID 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-WAR-2001; 20010S-0280067P.
29-WAY-2001; 20010S-0280068P.
16-WAY-2001; 20010S-0291280P.
17-WAY-2001; 20010S-0291829P.
17-WAY-2001; 20010S-0291849P.
19-UNN-2001; 20010S-0291849P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2002; 2002WO-US009944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0300001P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
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                                                                                           49; Conservative
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Dufour GE, Hillma...
Daugherty SC, Dam TC, I
Peralta CH, David MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis; hepatitis.
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                                             Query Match
Best Local Similarity
Sequence 548 AA;
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                                                                                                                                                                                                                                                                                    155
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                                                                      Best Loc
Matches
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, catteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antianaemic, antianaemic, antianaemic, antipsoriatic and heparotropic activity. The polymucleotides of the invention can be used for gene therapy, of protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, lumphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's cliefactive disorders (e.g. cancers including adenocarcinoma, lumphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's syndromes, inflammation, osteoporosis, thrombocycopaemia, psoriasis or hepatitis. ABUI1450-ABUI1845 represent the MDDT polymucleotides encoded by ABUI1450-ABUI1845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    764 DKDRKDLEGRLKAR----EDLLLPIYHQVAVQFADFHDTPGRMLEKGVISDILEWKTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-----THVISDIQDFVVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIDPMKVPDHADKFERHVGIVDFKGEL------AMRNIEARGLKOMKRQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 953;
                                                                                                                                                                Claim 27; SEQ ID NO 465; 339pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 S-----LEISDEGNITMTSFEVROFANVVNHIGGLSIL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human drug metabolising enzyme, DME-2, SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 82.5; C
24.2%; Pred. No. 22;
tive 32; Mismatches
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us-10-024-955-7.rag

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-ANU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                     Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression, immune stimulation; anti-inflammatory; leukaemia.
Novel human secreted protein #3339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 678; 765pp; English.
                                                                                                                                                                                                                                                                 16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                         18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2486 AA;
                                                                                                                                                                            WO200179449-A2
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                       25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
DNE-1 to DNE-13 (ABPS9210-ABPS921) and their coding metabolishing the present of the sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME.

Dreventing disorders associated with aberrant expression of DME, particularly cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopenia or cancer), developmental disorders (e.g. osteoporosis, thrombosis, diabetes), eye rardation), endocrine (e.g. osteoporosis, thrombosis, diabetes), eye cystic fibrosis), gastronitestinial disorders (e.g. gastroenteritis, diarrhoea), liver disorders (e.g. ADS, allergies, asthma, autoimmune/inflammatory disorders (e.g. ADS, allergies, asthma, autoimmune/inflammatory disorders (e.g. ADS, allergies, asthma, glammatory disorders (e.g. ADS, allergies, asthma, allergies, stymbone, contoinment thyroiditis, contact dermatitis, croh's disease, glomerulonephritis, Goodpasture's syndrome, multiple sclerosis, osteoarthritis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, syndrome, uveitis, They are also useful in the assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of DME. The polynucleotides encoding DME are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABZ81301-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid sequences of \overline{\mathrm{DMS}}. The polynucleotides encoding DME are useful for creating transgenic animals to model human disease
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to novel human drug metabolising enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Gaps
                                                                                                                                                                                                 Li JX;
Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                            New drug metabolizing enzymes (DME) useful for diagnosing, treating preventing diseases or conditions associated with aberrant DME expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma, hepatitis or osteoporosis.
                                                                                                                                                                                               Ramkumar J, Emerling BM, Richardson TW, Li JX;
Honchell CD, Baughn MR, Tang YT, Lee EA, Elliott VS
S, Swarnakar A, Forsythe IJ, Sanjanwala MM, Yao MG;
Y, Gorvad AE, Becha SD, Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 2458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 82.5; Di
24.2%; Pred. No. 85;
cive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 149-155; 181pp; English.
                                        06-JUL-2001; 2001US-0303745P.
13-JUL-2001; 2001US-0305402P.
13-JUL-2001; 2001US-0305158P.
14-SEP-2001; 2001US-0322127P.
05-JUL-2002; 2002WO-US021105
                                                                                                                                                       (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2458 AA;
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                                                                                                                                                                                                                                            Yue H, Lee S,
Zebarjadian Y,
                                                                                                                                                                                                 Griffin JA,
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Drmanac RT;

Liu

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----THVISDIQDFVVAL
                                                                       ----AMRNIEARGLKOMKROG----
   DB 4; Length 2486;
                                                                                                                                                                                                                                 S-----LEISDEGNITMTSFEVROFANVVNHIGGLSIL 175
                                                                                                                                         DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT
                                    49;
7.7%; Score 82.5; D
24.2%; Pred. No. 87;
tive 32; Mismatches
                                                                     45 TIDPMKVPDHADKFERHVGIVDFKGEL-----
                                                                                                                                                                                                                                                                                                                                 ABB84649 standard; protein; 2487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                    39; Conservative
                    Local Similarity
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                                                                                                                                         89
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   Query Match
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                                                                                                                                                                        임
                                                                                                      2268
                                                                                                                                                             2269 DXDRKDLEGRLKAR----EDLLLPIYHOVAVOPADFHDTPGRMLEKGVISDILEWKTAR 2323
                                                                                                                                         142
                                                                         88
                                                                                             2210 TINPLCIEMYADK-ESRGGVLEPEGTVEIKFRKKDLIKSMRIDPAYKKLMEQLGEPDLS
                                                                                                                                         ----THVISDIQDFVVAL
                                                                       45 TIDPMKVPDHADKFERHVGIVDFKGEL------AMRNIEARGLKQMKRQG----
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AAU32848 standard; protein; 2486 AA

18-DEC-2001

DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT

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hepatotropic, cytostatic, anti-HIV; antiallergic, antiasthmatic, cancer, antianaemic; antidiabetic, antiinflammatory; neuroprotective; antiulcer; antithematic; antiarthic; cardiant; hypotensive; gonadal dysgenesis; vasotropic, antiarthitic; cardiant; hypotensive; gonadal dysgenesis; antiparkinsonian; ophthalmological; cell proliferative disorder; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; andioracitis; authoroscis; dirensis; happitis; angina pectoris; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocardial infarction; Huntington's disease; myocarditis; neurological disorder; cataract; developmental disorder; Duchenne muscular dystrophy; antipsoriatic; Becker muscular dystrophy; Cushing's syndrome.
                         Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;
Human SECP-1 protein from clone 7757335CD1 SEQ ID 1.
                                                                                                                                                                                                                                                                                                                   30-MAR-2001, 2001US-0280527P.
06-ARR-2001, 2001US-0282112P.
09-ARR-2001, 2001US-028385P.
13-ARR-2001, 2001US-0343718P.
19-GCT-2001, 2001US-0343718P.
17-DEC-2001, 2001US-0339236P.
13-FBB-2002, 2002US-0357002P.
                                                                                                                                                                                                                                                                                              29-MAR-2002; 2002WO-US009820
                                                                                                                                                                                                                                                                                                                                                                                                                                [INCY-] INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABS57545
                                                                                                                                                                                                                                         WO200279441-A2
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                   10-OCT-2002
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This invention describes novel secreted proteins (SECP) which have antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic, antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic, antiathmator, antialleragic, antiathmatic, antiathmatic, antiathmatory, neuroprotective, antipathisociae, antipachiae, antipathisociae, vasotropic, antiarthritic, cardiant, hypotensive, anticonvulsant, nootropic, immunosuppressive, antipathisociae, anticonvulsant, cardivity. The polymucleotides and polypeptides of the invention can be used for diagnosing, treating or preventing cell proliferative disorder. e.g. arterioscelerosis, athrensolerosis, dirthosis, hepatitis, cancer, autoimmune/inflammatory disorderse.g. acquired immunodeficiency syndrome (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease, autoimmune/inflammatory disorder e.g. acquired immunodeficiency syndrome (AIDS), allergies, ulcerative colitis, psoriaeis, rheumatoria argina pectoris, precipated anticipated in the content of disease, myocardial infarction, angina pectoris, hypertension, Raymaud's disease, myocardial infarction, angina pectoris, contentolated disorders e.g. buleband and Becker muscular dystrophy.

Contention can also be used Crotuselell-Jakob disease, etc; and developmental disorders e.g. Duchenne and Becker muscular dystrophy, cataract, gonadal dysgenesis, Cuching's syndrome, etc. The products of the invention can also be used the animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in channel, carrier or affected individuals, and as hybridization probes for normal, carrier or affected individuals, and as hybridization probes for Jan BM, Elliott VS, Forsythe IJ;
He A, Honchell CD, Ison CH;
Ason PM, Sanjanwala MM;
Thangavelu K, Tran UK, Walia NK; Novel human secreted protein useful for treating, preventing or diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus, anemia, epilepsy, cataract, Alzheimer's disease. Baughn MR, Burford N, Ding L, Duggan BM, Igandhi AR, Gietzen KJ, Griffin JA, He A, Isal PG, Lee ES, Lee S, Lu DAM, Mason PM, Ramkumar J, Tang YT, Thangave Warren BA, Yao MG, Xu Y, Yue H; Claim 56; Page 143-149; 188pp; English. WPI; 2003-058429/05.

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7;
                                                                                                                                   2239 TINPLCIEMYADK-ESRGGVLEPEGTVEIKFRKKDLIKSMRRIDPAYKKLMEQLGEPDLS 2297
                                                                                                                                                                             NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
                                                                                                                                                                 89 DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT----THVISDIQDFVVAL
                                                                                                                    45 TIDPMKVPDHADKFERHVGIVDFKGEL-----AMRNIEARGLKOMKROG----
                                                                                              Gaps
mapping naturally occurring genomic sequences. ABB84649-ABB84673 represent secreted proteins encoded by the cDNA's shown in ABS57545-ABS57569, described in the disclosure of the invention
                                                                                              41;
                                                                    7.7%; Score 82.5; DB 6; Length 2487;
24.2%; Pred. No. 87;
ve 32; Mismatches 49; Indels 41;
                                                                                                                                                                                                                            : | : | : | | 1 | 2353 TFLYWRLRRLLLEDQ-----VKQEILQASGELSHVHIQSML 2388
                                                                                                                                                                                                               143 S------LEISDEGNITMTSFEVRQFANVVNHIGGLSIL 175
                                                                                                                                                                                                                                                                                              ABU65149 standard; protein; 2498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0274101P.
2001US-0274194P.
2001US-0274281P.
2001US-0274322P.
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2001US-0275235P.
2001US-0275578P.
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2001US-0275601P.
2001US-0276000P.
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2001US-0276994P.
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2001US-0280900P
                                                                                 24.2%;
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                  Human NOV76a protein.
                                                                                    1 Similarity
39; Conserv
                                                  Sequence 2487 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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12-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001;
08-MAR-2001;
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02-APR-2001;
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                                                                       Query Match
Best Local S:
Matches 39,
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2001US - 0283475P
2001US - 0287424P
2001US - 0286342P
2001US - 0286328P
2001US - 0291190P
2001US - 0291190P
2001US - 0291489P
2001US - 0294889P
                                                                                                                              2001US-0312903P.
2001US-0318462P.
2001US-0318770P.
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2001US-0325681P.
2001US-0330380P.
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2001US-0332271P.
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2001US-0333272P.
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2001US-0337426P.
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                                                                                                                                                                                                                                                                                                                                   Rieger DK;
                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                  2002-723332/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma. The product vaccine. ABU6504ABX97008-ABX97185
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABX97116.
                                                                                                                                                                            31-OCT-2001;
14-NOV-2001;
                                                                                                                                                                                                                                                                07-MAR-2002;
                                                     16-MAY-2001;
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                                                                                                                                                                                                                          21-NOV-200
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                                                                           31-MAY-2
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Anderson D; a CEA, Li L; Kekuda R; Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CBA, Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V, Epernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, A NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.

Claim 1; Page 313-314; 1103pp; English.

This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity esq. cancer, hypotension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65218 represent the NOVX polypeptides encoded by

Sequence 2498 AA;

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7
                                                                                      88
                                                                                    --AMRNIBARGLKOMKROG----
                                           49; Indels 41; Gaps
      DB 5; Length 2498;
Query Match
7.7%; Score 82.5; D
Best Local Similarity 24.2%; Pred. No. 87;
Matches 39; Conservative 32; Mismatches
                                                                                    TIDPMKVPDHADKFERHVGIVDFKGEL-
                                                                                    45
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7;

Gaps

30;

39; Indels

27; Mismatches

24.48;

31; Conservative

Best Local Similarity Matches 31; Conserv

Query Match

7.7%; Score 82; DB 4; Length 277; 24.4%; Pred. No. 4.3;

AAH52104 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the collypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymorleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polymucleotide sequences given in the capture olisting of the present invention, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given the present of the pres | : | | | | | | | | DYDRKDLEGRLKAR----EDLLLPIYHQVAVQFADFHDTPGRMLEKGVISDILEWKTAR 2363 2250 TINPLCIEMYADK-ESRGGVLEPEGTVEIKFRKKDLIKSMRIDPAYKKLMEQLGEPDLS 2308 ----THVISDIQDFVVAL 142 Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis. S. epidermidis open reading frame protein sequence SEQ ID NO:1988. : | : | : | : | : | 2364 TFLYWRLRRILLIEDQ-----VKQEILQASGELSHVHIQSML 2399 143 S-----LEISDEGNITMTSFEVRQFANVVNHIGGLSIL 175 DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-Claim 18; Page 540; 2188pp; English. AAG82447 standard; protein; 277 09-NOV-2000; 2000WO-US030782 99US-0164258P Staphylococcus epidermidis for SEQ ID NO:4455 to 4464 03-SEP-2001 (first entry) (GLAX) GLAXO GROUP LTD WPI; 2001-316495/33. N-PSDB; AAH53297. Sequence 277 AA; WO200134809-A2 6661-VON-60 endocarditis. Kimmerly WJ; 17-MAY-2001 89 2309 AAG82447; RESULT 87 à

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196 KEMTKVLAPAFKRE 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to movel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepais in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 QDFVVALSLEISDEGNITMISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVR 195
                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 DANVKGEEGIVKAHLLIGVHDDIVSME------YDLAYKLGDLHPT-THVISDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 DGNILIPQGVINELQIVADSNDSVKREKGKRGLDILNELYDLDYPTKVIHPTKTH--SDI
MKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL
                         173 AQQY--HAHVITTDFNL----NKVCHVQGITALN-----VNDLSBAIKPNVHQGDQLSIL
                                                                                          143 SLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3434; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus protein #1717.
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                                                                                                                                                                                                                                                                                                                                                      ABM72477 standard; protein; 357 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-IB002637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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                                                                                                                                                                                         203 APAFKRE 209
                                                                                                                                                                                                                                   222 LTKIGKE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-120786/11.
N-PSDB; ACF74037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 357 AA;
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Best Local Simi
Matches 32;
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ABM72477
ABM7247
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 AQQY--HAHVITTDFNL----NKVCHVQGITALN-,----VNDLSEAIKPNVHQGDQLSIL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 MKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4057.
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7.7%; Score 82; DB 5; Length 362;
Best Local Similarity 24.4%; Pred. No. 6.4;
Matches 31; Conservative 27; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4057; 267pp; English.
                                                                                                                                                                                 ABP39212 standard; protein; 362 AA.
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97US-0064964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy
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290 GDQLHILIKMGKE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermidis.
                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
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RESULT

Chlamydia; lpdA; infection; diagnostic; medicament;

therapy; antibacterial

gene

Chlamydophila pneumoniae

WO200121802-A1

29-MAR-2001

C. pneumoniae lpdA protein

(revised)
(first entry)

11-SEP-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharymgitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE------RH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGFAAIVSHEITQQILGAYVIGPHASSLIGEMTL----AIRNELT 361
                                                                                                                                                                                    Chlamydia pneumoniae transmembrane protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 1240-1241; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Chlamydia pneumoniae.
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AAB62188
ID AAB62188 standard, protein, 461 AA.
                        AAY35476 standard; protein; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-00014673.
98US-0107078P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-IB001890
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                       Chlamydophila pneumoniae.
                                                                                                                   (revised)
                                                                                                                                                                                                                                                                           neutralising epitope.
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1997;
                                                                                                              17-OCT-2003
13-SEP-1999
                                                                     AAY35476;
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AAY35476

AAY35476

AAY35476

AAY3

AAAY3

AAAX3

AAAY3

AAAY3

AAAY3

AAAY3

AAAY3

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11;
                                                                                                                                                                                                                                                                                                  Novel Chlamydia pneumoniae 1pdA protein and polynucleotides encoding them useful as component of vaccines for treating Chlamydia infections, and for detecting Chlamydia infection in the body fluid of a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This represents the Chlamydia pneumoniae lpdA protein. The lpdA protein can be expressed by standard recombinant methodology. The lpdA protein, polyuucleotide and antibodies specific to the protein and vaccines comprising the lpdA protein are useful for preventing or treating Chlamydia (C. trachomatis, C. psittaci, C. pneumonia or C. pecorum) infection. Vaccine vectors, and the lpdA protein are useful in the preparation of medicaments for preventing and/or treating Chlamydia infection. Primers and probes derived from the lpdA gene are also useful for detecting and/or identifying Chlamydia in the biological material. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VGIV-DFKGELAMRNIEARGLKOMKROGD-----ANVKGEEGIVKAHLLIGVHDDIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 AGVIRDDRGVIPVDETMRTNVPNIYAIGDITGKWLLAHVASHQGVIAAKNISGHHE---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-
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20.4%; Pred. No.
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                                                                                                                                                                 Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Fig 1; 78pp; English
5-SEP-2000; 2000WO-CA001086.
                                                       99US-0154325P
                                                                                                         (AVET ) AVENTIS PASTEUR LTD.
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Best Local Similarity 20.10.
The 46; Conservative
                                                                                                                                                                 Comen RP,
                                                                                                                                                                                                                      2001-257992/26.
                                                                                                                                                                                                                                                   N-PSDB; AAF57425
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                                                    17-SEP-1999;
                                                                                                                                                              Murdin AD,
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ABB94271
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ABU27059;

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The present invention describes compositions comprising a Chlamydia Capi protein and methods for the diagnosis and therapy of Chlamydia infection. Chlamydia DNA and protein sequences from the present invention can have antibacterial and immunostimulant activities, and can be used in vaccines. Compounds from the present invention can be used for eliciting an immuno response, specifically stimulating a Chlamydia-specific. T-cell response or inhibiting the development of a Chlamydia infection in an presence of Chlamydia in patient; to stimulate and/or expand T cells specific for a Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia in a patient; and for treatment of a Chlamydia in fection in an prisection. ABL92709 and ABB94096 to ABB94374 represent sequences used in the exemplification of the present invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                             Chlamydial infection, Chlamydia, vaccine, detection, diagnosis, antigen, antibacterial; immunostimulant, immune response,
Chlamydia-specific T-cell response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compositions comprising Chlamydia Capl protein and its use in the treatment of Chlamydia infection.
                                                                          Chlamydia pneumoniae protein sequence SEQ ID NO:399.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Probst P, Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 361-363; 537pp; English
                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001WO-US023121.
                                                                                                                                                                                                                                                                                                                                              20-JUL-2000; 2000US-00620412.
23-APR-2001; 2001US-00841132.
                  (revised)
(first entry)
                                                                                                                                                                                       Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179901/23.
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                29-AUG-2003
05-JUN-2002
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275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | |: | : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | | : | | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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Query Match 7.7%; Score 82; DB 5; Length 461; Best Local Similarity 20.4%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
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                                                                                                                                                                                     69; Indels
                                                                                                                                                                                               44; Mismatches
                                                                                                                                                                                               Conservative
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the foll antienness given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(2) a vector comprising a promoter operably linked to the nucleic acid

(2) a host cell containing the vector; (3) an isolated

conjugation or its fragment whose expression is inhibited by the antisense

continued or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

continued or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

continued or its fragment whose expression is inhibited by the proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for collular proliferation or the biological pathway required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibictic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibictic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture confidentifying proteins or screening for homologous nucleic acids are useful for confident discussion or for screening confidence acids are useful for the confidence or collection of an organism. The antisense nucleic acids are useful for the confidence or collection of single confidence and determination of an organism. The antisense model or callection and confidence or collections or for some p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained it alectronic format directly from WIPO at the printed specification, but was obtained fitp who, int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                          Protein encoded by Prokaryotic essential gene #12586.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 54983; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
                                                                         (first entry)
                                                                                                                                                                                                                           Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                                                                                                                                                                                                                                                                               WO200277183-A2.
                                                                         19-JUN-2003
                                                                                                                                                                                                                                                                                                                                   03-OCT-2002,
                                              23-OCT-2003
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Wall D,
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Sequence 461 AA;

Length 461; 9 DB 7.7%; Score 82;

ABU27059 standard; protein; 461 AA

RESULT 93 ABU27059 ID ABU2 XX

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11;
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                                                                                                                                                                                                                                                                                                                                                                               Recombinant, endotoxin, neutralisation, RENP; NCV139; lipopolysaccharide, LDS; bactericidal, permeability; increase; BPI; detection, Gram-negative; bacterium, infection, prevention; treatment; disorder; mediation; stimulation, neutrophil; monounclear cell; inhibition; shock; anemia; anaemia; disseminated intravascular coagulation; thrombocytopenia; thrombocytopaenia; adult respiratory distress syndrome; ARDS; renal failure; liver disease; half life; human.
                                                                                                                                                                 333 MDYSAIPSVIFTHP-----EIAMVGLSLQEAEQQNLPAKLTKFPFKAIGKAVALGAS 384
                                                       62 VGIV-DFKGELAMRNIEARGLKQMKRQGD-----ANVKGEEGIVKAHLLIGVHDDIVS
                                                                                                       114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ------
                 Gaps
                : 99
                                                                                                                                                                                                          385 DGFAAIVSHEITQQILGAYVIGPHASSLIGEMTL----AIRNELT 425
                                                                                                                                                                                            --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                        DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-----
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "wild type Lys replaced by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "wild type Lys replaced by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "wild type Lys replaced by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "wild type Lys replaced by Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "wild type Lys replaced by Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "wild type Lys replaced by Glu"
                                                                                                                                                                                                                                                                                                                                                         endotoxin neutralising polypeptide NCY139.
                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "wild type Lys replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild type Lys replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "wild type Arg replaced
  ed. No. 9;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l. .31
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                AAW16827 standard; protein; 487 AA.
                44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US006134
                                                                                                                                                                                                                                                                                                                                  (first entry)
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                  28-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                          AAW16827
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AAW16827
ID AAW16
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopaenia, adult respiratory distress syndrome, renal failure, liver disease and conditions associated with Gram negative bacterial infection. The RENP has an enhanced serum half life relative to naturally occurring BPI, and binds LPS without triggering a significant, undesirable immune response. N. B. Sequence not given in specification, but produced using the wild type hBPI sequence given in figure 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GKPTITCSSCSSHI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational profiling, expressed protein tag, BPT, kinase, phosphatase, protease, protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIVDFXGELAMRNIEAR------GLKQMKRQGDANVKGEEGIVKAHLLIGV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 HDDI----VSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFA 163
                                                                                                                                                                                                     The present sequence is the recombinant endotoxin neutralising bolypeptide (RENP) B(GAT9) (NCY139), which comprises the human bactericidal/permeability increasing protein (hBFI) mutant Lys148Gly, Lys150Asp, Lys160Asn, Lys161Gln, Arg167Gln, Lys169Val, Lys17Met, Lys1818Asp, Lys180Glu. The RENP, which selectively and specifically binds lipopolysaccharide (LPS) and has endotoxin neutralising activity, can be used to detect a site of Gram negative bacterial infection, and prevent or treat endotoxin related disorders, preferably where LPS mediated stimulation of neutrophils and mononuclear cells is inhibited, e.g. shock, disseminated intravascular coagulation, anaemia, rest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                           Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 VLVAIGTAVTAAVNPGVVVRISQKGEDYASQQGTAALQKE--LKRIKIPDYSDSFKIKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 G----KGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLIAAVAFVAVSADPIHYDKITEE-INKAIDDAIAAIEQSETIDPMKVPDHADKFE-RHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 NVVN-HIGGLSI-----LDPIFGVLSDVLTAIFQDIVRKEMTKVLAPAFK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 82; DB 2; Length 487; 20.7%; Pred. No. 9.7; ive 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 NFDLSIEGMSISADL -- KLGS-NPTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human expressed protein tag (EPT) #1218.
                                                                                                                                                                 Example 1; Page; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 20.7%
Matches 48; Conservative
Marra MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200278524-A2
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Scott RW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU04552
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ABU04552
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28-MAR-2002; 2002WO-US009671.

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tragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammadamia mimmunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide is also to solve the interpretation compounds that binds to a naturally processed class I or class II MRC-binding polypeptide. The polypeptides and polymentacions, concer, gastric cancer, adenocarcinoma, marcoma, melanoma, mymboma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, important the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIVDFKGELAMRNIEAR------GLKQMKRQGDANVKGEEGIVKAHLLIGV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G----KGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDDI----VSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                             New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LLIAAVAFVAVSADPIHYDKITEE-INKAIDDAIAAIEQSETIDPMKVPDHADKFE-RHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKE--LKRIKIFDYSDSFKIKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention describes a purified polypeptide, which comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 NVVN-HIGGLSI-----LDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein involved in intermediate metabolism of nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7%; Score 82; DB 6; Length 487;
20.7%; Pred. No. 9.7;
.ive 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                               New polypeptides (e.g. kinases, phosphatases, cytoskeletal proteins, receptors or transcript
                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 1218; 134pp; English.
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                                                                                                                                                                                                  Urban RG;
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              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
04-DEC-2001; 2001US-0336370P.
04-DEC-2001; 2001US-0336880P.
20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                  Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 20.7
les 48; Conservative
                                                                                                                                                                                                                                      WPI; 2003-040607/03
                                                                                                                                                            (ZYCO-) ZYCOS INC.
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                                                                                                                                                                                                  Chicz RM,
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GDYVILHGKLTVYAPRGQYQIVAYALTFSGEGNL-----LQQFEERKQRLAAEGYFDPK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, bartholinitis, pneumcpathy, venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD------IVSMEYDLAYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 NVSLQTSG-------HLYFAIKDSKAVLNGAFFHFRSKYFDRKPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EPLYLQRISYPLYNKSISHN-SHVPMSITSPPIEVSVLTDSIKNLLEKNFLRVVVKGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DPIHYDKITEEI-NKAIDDAIAAIEQSETIDPMKVPDHADK----FERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 GD---LHPTTHVISDIQDF-VVALSLEISDEGNITWTSFEVROFANVVNHIGGLSILDP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 82; DB 2; Length 530;
21.6%; Pred. No. 11;
ative 32; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IFGVLSDVLTAIFQDTVR 195
                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 731; 1755pp; English
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                                                                                                                                                                                        97FR-00015041.
97FR-00016034.
98US-0107077F.
                                                                                                                                                            98WO-IB001939
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                                                                                                                                                                                                                                                                                                                  WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 530 AA;
                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                            27-NOV-1998;
                                                                                                                                                                                          28-NOV-1997;
17-DEC-1997;
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                                                                                                 409928475-A2
                                                                                                                                10-JUN-1999
                                                                                                                                                                                                                                                                                      Griffais R;
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Matches
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Human; primer; detection; diagnosis; antisense therapy; gene therapy.

28-JUL-2000; 2000EP-00116126.

EP1074617-A2

07-FEB-2001.

27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899

(HELI-) HELIX RES INST.

Human protein sequence SEQ ID NO:14186.

26-JUN-2001

AAB94036;

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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonuclectide comprises one of the 5602 complementary strand of a polynuclectide which comprises one of the 5602 oligonuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprises a sequence complementary to the comprises a sequence complementary to the sequence and an oligonuclectide comprising a sequence complementary to the polynuclectide comprises a 3'-end sequence of an oligonuclectide which comprises a 1'-end sequence of complementary to a polynuclectide which comprises a 1'-end sequence of sequence of sequence of sequence of sequence of 3'-end sequence of se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID NO 14155; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                        27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                           28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T,
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     Homo sapiens.
                                                     EP1074617-A2
                                                                                                                                                                                                              29-JUL-1999;
                                                                                                        07-FEB-2001
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Ishii S,
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VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHA-DKFERHVGIV---DFKGE 70 Query Match 7.7%; Score 82; DB 4; Length 767; Best Local Similarity 22.9%; Pred. No. 18; Matches 36; Conservative 30; Mismatches 55; Indels

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599

LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA------ 119 600 ----VYPFGIVGMANKGDCLQKGES--VKFQLCV-LGQNAQTMAYNITPLRRATVECVK 651

-----YKLGDLHPTTHVISDIQDFVVALSLEISDE 149 DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE 652

8 엄

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. Yamamoto J; Saito K, Ya Otsuki T, Nishikawa T, Hayashi K, S T, Wakamatsu A, Nagai K,

Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length WPI; 2001-318749/34.

Claim 8; SEQ ID NO 14186; 2537pp + Sequence Listing; English.

Yamamoto J;

Saito K, Otsuki

sogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K,

Ota T, Is Ishii S,

The present invention describes primer sets for synthesising 5602 full
[1] In oligo-of primer and an oligonucleotide complementary to the

[2] Complementary strand of a polynucleotide which comprises one of the 5602

[3] Complementary strand of a polynucleotide which comprises one of the 5602

[3] Complementary strand of a polynucleotide which comprises a combination

[3] Complementary strand of a polynucleotide which comprises a 5'-end

[4] Complementary strand of a polynucleotide which comprises a 5'-end

[5] Sequence and an oligonucleotide comprising a sequence complementary to the

[5] Complementary strand of a polynucleotide which comprises a 5'-end

[5] Sequence and an oligonucleotide comprises a 3'-end sequence, where the complementary to a

[5] Sequence and an oligonucleotide comprises a 3'-end sequence, where the complementary to a

[6] Sequence and an oligonucleotide comprises a 1'-end sequence, where these the complementary to a

[6] Sequence and an oligonucleotide comprises a 1'-end sequence, where these complementary to a

[7] Sequence and an oligonucleotide comprises a 1'-end sequence, where the combination of

[7] Coligonucleotide comprises a 1'-end sequence, where these complementary to a

[8] Sequence and sequence are useful for synthesising polynucleotides,

[8] Coligonucleotide comprises of the abnormality of the proteins encoded by

[8] Coligonucleotides, all of which are used in the exemplification of the

[8] Coligonucleotides, all of which are used in the exemplification of the

Sequence 767 AA;

70 15 VSADPIHYDKITEBINKAIDDAIAAIBQSETIDPMKVPDHA-DKFERHVGIV---DFKGE Gaps 71 LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-4; Length 767; 7.7%; Score 82; DB (22.9%; Pred. No. 18; ve 30; Mismatches 22.9%; Conservative Query Match Best Local Similarity Matches 36; Conserv

à d ò 600 ----VYPFGIVGMANKGDCLQKGES--VKFQLCV-LGQNAQTMAYNITPLRRATVECVK 651

AAB94036 ID AAB94036 standard; protein; 767 AA.

RESULT 98

---EVROFANV-----VNHIGGLSIL 175

59

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168 SLELEIIICYLLLDKLIEPHASPKYLIIDEVQDNSVFEFVFALRPAKHNTSLYLVGDSS 227
                                                      288 ANSF----DAPTADSFKEKVBLDMHHV 310
                                                                                        176 DPIFGVLSDVLTA-IFQDTVRKEMTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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N-PSDB; ABL02886.
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                                      152 ITMTSF-
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                                                                                                                                                                                                                                                                                                pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.
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                                                                                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and analysing a homologue of a gene derived from coryneform bacterium. Vitanis, saccharides and organic acids, nucleic acids, vitanins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIVDFK-GELAMRN---IEARGL--KQMKRQGDANVKGEEGIVKAHL--LIGVHDDI--V 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SME-----YDLAYKLGDLH--PTTHVISDIQD-----FVVAL-----SLEISDEGN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 IAVLSFTNAAADNITAKNDKVTSMTISKMVHEIYA------HNFPDHEISTIDTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 IAAVAFVAVSADPI--HYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDH-ADKFERHV
                                                                                                                                                                                                                                                                                                                                                                                                                             Yokoi H;
                                                                                                                                                                                                         bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; SEQ ID NO 5445; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 82; DB 4; Length 785; 23.6%; Pred. No. 19; ve 38; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Ochiai K,
                               Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                -----YKLGDLHPTTHVISDIQDFVVALSLEISDE
                                                                                                                                                                                 C glutamicum protein fragment SEQ ID NO: 5445.
                                                                                                     AAG91691 standard; protein; 785 AA
                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                              2000JP-00159162
2000JP-00280988
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                                                                                                                                                                                                                                               Corynebacterium glutamicum.
                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                   organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH66910
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03-AUG-2000;
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Tateishi N,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ16176-ABIJ3011), expressed DNA sequences (ABID1840-ABIJ40175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 BEINKAIDDAIAAIEQS------ETIDPM---KVPDHADKFERHVGIVDFKGELAMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 3141; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 3141.
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7.6%; Score 81.5; DE
Best Local Similarity 22.5%; Pred. No. 3.7;
Matches 36; Conservative 29; Mismatches
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ABB58783 standard; protein; 227
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US-09-107-532A-8512

US-09-107-532A-9510

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US-09-561-818A-12

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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-553-336A-7

US-08-462-778-62-8

US-08-973-462-8

US-08-336-618-12

US-08-336-618-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-393-888-2

US-09-137-175A-9

US-09-137-175A-9

US-09-488-52A-197

US-09-488-52A-110

US-09-489-52A-110

US-09-107-53A-578

US-09-107-53A-578

US-09-107-53A-100

US-09-108-455A-894

US-09-1194-401C-4657

US-09-468-041-2

                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                         protein search, using sw model
                                                                                                                           6, 2004, 15:59:26
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                           August
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81.5
81.5
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Perfect score:
                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                              Total number
                                                                                           protein
                                                                                                                                                                                                                                 Seguence:
                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
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61 HVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 213;
                                                                                                              Sequence 7, Application US/08553336A
Patent No. 6413738
GENERAL INFORMATION:
APPLICANT: Wayne R. Thomas and Kaw-Yan Chua
TILLE OF INVENTION: Allergenic Proteins and Peptides From
TILLE OF INVENTION: House Dust Mite and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1996
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 08/081,540
FILING DATE: 22-JUNE-1993
ATTORNEY/AGENT INPORMATION:
NAME: 21-JUNE-1993
ATTORNEY/AGENT INPORMATION:
NAME: Alane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/POCKET NUMBER: IMI-032CP2
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1068; DB 4;
100.0%; Pred. No. 1.5e-113;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
ALIGNMENTS
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 213 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-553-336A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                               STATE: Ma
                                                                                        JS-08-553-336A-7
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RESULT 2 US-08-553-336A-2 ; Sequence 2, Application US/08553336A ; Parent No. 6413738

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121 KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HIGIIDLKGELDMRNIQVRGLKOMKRVGDANVKSEDGVVKAHLLVGVHDDVVSMEYDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSDKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
APPLICANT: Wayne R. Thomas and Kaw-Yan Chua TITLE OF INVENTION: Allergenic Proteins and Peptides From TITLE OF INVENTION: House Dust Mite and Uses Therefor NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08462778
| Patent No. 6077517
| GENERAL INFORMATION:
| APPLICANT: Thomas, Wayne R. APPLICANT: Thomas, Wayne R. TITLE OF INVENTION: Allergenic Protein and Peptides From TITLE OF INVENTION: Allergenic Protein and Peptides From TITLE OF INVENTION: Allergenic Protein and Uses Therefor NUMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESSE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: CORFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.1%; Score 962; DB 4; Length 21 Best Local Similarity 85.9%; Pred. No. 1.9e-101; Matches 183; Conservative 18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSTRICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/081,540
FILING DATE: 22-JUNE-1993
ATONEY/AGENT INFORMATION:
NAME: Ane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 38,872
REGISTRATION NUMBER: 38,672
REJECOMMUNICATION INFORMATION:
TELEFONE: (617)227-7400
TELEFPAX: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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US-08-462-778-2
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CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
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US-08-336-618-12
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; Factor No. 6191270
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALARIAL PRE-ERTHROCYTIC STAGE POLYPEPTIDE MOLECULES
CURRENT TILING DATE: 1998-02-06
EARLIER FILING DATE: 1998-06-12
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATCHING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 215;
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,778
FILING DATE:
                                                                                                                                                                                                                                                                                                                                    IPC-053CP (IMI-032CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

89.8%; Score 959; DB 3; I
Best Local Similarity 85.4%; Pred. No. 4.1e-101;
Matches 182; Conservative 19; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                   CLASSIFICATION 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 12 March 1993
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. Mandragouras
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 617-227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 215 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                          1084 -----EQNV-YVDVDVPAMKDQFLGIINEAGGLKEMFFNLEDVFKSESDVITVEBIKD 1135
                                                                                                                                                                                                                                                                                                                       82 KOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                 142 LSLEISDEGNITMISFEV----ROFANVVNHIGGLS----ILDPIFGVLSDVLTA--IFQ 191
                                                                                                                                                                                                      22 YDKITEEINKAIDDAIAAIEQSETIDPWKVPDHADKFERHVGIVDFKGELAMRNIEARGL 81
                                                                                                                                                  Gaps
; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide US-08-973-462-8
                                                                                                                                                  34;
                                                                                     Query Match
8.4%; Score 90; DB 3; Length 1786;
Best Local Similarity 23.3%; Pred. No. 1;
Matches 47; Conservative 43; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brook, Smith and Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1991
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
REOR APPLICATION DATA:
APPLICATION NUMBER: CS/07/77,752
FILING DATE: 10-OCT-1991
REOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: US 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1136 EPVOKEVEKETVSIIE-EMEEN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 DIVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNES/CARACTOR PARTICIA
REGISTRATION NUMBER: 32,227
REPRENEC, POCKET NUMBER: VE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 459 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Peattie, Debra A. APPLICANT: Harding, Matthew APPLICANT: Livingston, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
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75 DKFSFDLGKGEVIKAWDIAIATMKVGEVCHITCKPEYAYGSAGSPPKIPPNATLVFE--V 132
                                                                                                                                              63 GIVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKL 122
                                                                                                                                                                             18 IAMEEADVIVEVVSGKEGITDADETVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGDLHPTTHV----ISDIQDFVVALSLEISDEGNITMTSFEVRQFANV-----VNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 LGEPLPISSVHGIGTGDVLDAIVENLPNEYEËENPDVIKFSLIGRPNVGKSSLINAILGE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 AN-----SMEYDL----AHLLIGVHDDIV-----SMEYDL----AYK 121
                                                  -- DPMKVPDHAD-KFERHV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.2%; Score 88; DB 4; Length 393;
Best Local Similarity 21.8%; Pred. No. 0.17;
Matches 46; Conservative 34; Mismatches 89; Indels 42; Gaps
  17;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09393858
| Sequence 2, Application US/09393858
| Patent No. 6627747
| GENERAL INFORMATION:
| APPLICANT: Fritz, Christian
| APPLICANT: Graman, Philip
| APPLICANT: Graman, Luz-Maria
| TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
| FILE REFERENCE: 06266-088001
| CURRENT FAPLICATION NUMBER: US/09/393,858
| CURRENT FILING DATE: 1999-09-09
| PRIOR APPLICATION NUMBER: 60/099,578
| PRIOR APPLICATION NUMBER: 60/099,578
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09393858;
Patent No. 6627747;
GENERAL INPORATION:
APPLICANT: Fritz, Christian
APPLICANT: Guzman, Philip
APPLICANT: Gizman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 06266-080001;
CURRENT APPLICATION NUMBER: US/09/393,858;
CURRENT PRILIG DATE: 1999-09-09;
PRIOR APPLICATION NUMBER: 60/099,578
; RIGHT FILING DATE: 1998-09-09;
NUMBER OF SEQ ID NOS: 43
     Indels
     50;
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     25; Mismatches
                                                  18 DPIHYDKITEEINKAIDDAIAAIEQSETI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Streptococcus pneumoniae US-09-393-858-2
       Conservative
                                                                                                                                                                                                                                                                           |:
GE 194
                                                                                                                                                                                                                                          GD 124
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     Matches
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APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                               63 GIVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKL 122
                                                                                                                                                                     18 DPIHYDKITEEINKAIDDALAAIEQSETI------DPMKVPDHAD-KFERHV
                                                                                                                       17;
                                                                       8.3%; Score 88.5; DB 1; Length 459; llarity 24.6%; Pred. No. 0.19; Conservative 25; Mismatches 50; Indels 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
PRIDE APPLICATION DATA:
APPLICATION NUMBER: PCT/
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTOMNEY/AGENT INFORMATION:
AND APPLICATION NUMBER: PCT/
ATTOMNEY/AGENT INFORMATION:
AND APPLICATION NUMBER: PCT/
ATTOMNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPI91-06A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFRENCE/DOCKET NUMBER: VPI9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 677-861-6240
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
; MOLECULE TYPE: protein US-08-336-618-12
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                                                             Query Match
Best Local Similarity
Matches 30; Conser
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-336-618-26
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9, Application US/08137175A
Sequence 9, Applicatic
Patent No. 5777095
GENERAL INFORMATION:
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STATE: D.C
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US-08-479-017-9
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Patent No. 6551792

GENUEAL INFORMATION:

GENUEAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

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; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-22392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 IAMEEADVIVFVVSGKEGITDADEYVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 KVLDEARLAIDDARA------EHG-----EHG-----ELRGSLRVTTTQEYGLRQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 LGDLHPTTHV----ISDIQDFVVALSLEISDEGNITMTSFEVRQFANV----VNHIGGL 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                         Query Match
8.2%; Score 88; DB 4; Length 436;
Best Local Similarity 21.8%; Pred. No. 0.2;
Matches 46; Conservative 34; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                           i LENGTH: 436
i TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-393-858-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Conservative
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US-09-252-991A-22392
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RESULT 10 US-08-137-175A-9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 LIGVHDDI--VSME-YD-----LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGN 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HANSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Indels
                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                              ISEE: BROWDY AND NEIMARK: 419 Seventh Street, N.W., Suite 300 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 84.5; DB Best Local Similarity 22.3%; Pred. No. 0.28;
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FR: BARBOUR=1B
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-OCT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       SUCKINGARY APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175A
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08479017
Patent No. 6143872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 28,005
REFSERICE/DOCKET NUMBER: B7
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248633
INFORMATION FOR ESQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
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                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-498-520A-34

) Sequence 34, Application US/09498520A

) Patent No. 6613553

) GENERAL INFORMATION:

APPLICANT: Rock, Charles O

) TITLE OF INVENTION: No. 661353e1 Enoyl Reductases and Methods of Use Thereof

FILE REFRENCE: SJ-0022

) CURRENT APPLICATION NUMBER: US/09/498,520A

) CURRENT PILING DATE: 2000-02-04

) NUMBER OF SEQ ID NOS: 62

) SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                           121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 T----THVISDIODFVVALSLEISD------EGNITMISFEVROFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                   510 DILHKRVIGONDAVNSISKAVRRARAGLK-----DP-----KRPIGSFIFLGPTG 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 MRNIEARGLKOMKR-----QGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHP 127
                                                                                                                                                                                                                                                                                                           18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ARVLRTPFARKIQEMEFENPMQAEEMLVGSLRRAVVEGDLERGSFMVQQSAGLIDEI---
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                                                                                                                                                                                                                        7.9%; Score 84.5; DB 4; Length 823; 23.0%; Pred. No. 1.4; ive 35; Mismatches 87; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.9%; Score 84; DB 4; Length 314; Best Local Similarity 23.5%; Pred. No. 0.35; Matches 48; Conservative 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DKITEEINKAIDDAIAA--IEOSETIDPMKVPDHADKFERHV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 BLQDQRFAGFGGASEGSDYETVRKTMMKELKNSFRPE 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                         60/055,779
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                                                                                                                               TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Thermotoga maritima
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4081
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                              US-09-134-001C-4081
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LENGTH: 314
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                                                                                                               LENGTH:
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Patent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILLE OF INVENTION UNMERR: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 LIGVHDDI--VSME-YD-----LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGN 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
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                                                                                          E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.9%; Score 84.5; DB 22.3%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BARBOUR=1B
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-628-5197
                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 294 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.3$
Matches 52; Conservative
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: IMPRITITE OF INVENTION: PROI NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                             STREET: 419 Seve
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CLASSIFICATION:
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US-09-134-001C-4081
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TOPOLOGY:
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uccette-Stamm and David Bush
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LGDLHPTTHVISDIQDFVVALSLEISDEGNITWTSFEVRQFANVVN---HIGGLSILDPI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Gaps
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18.7%; Pred. No. 1.2;
tive 36; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION STREET: 1.00 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
;
; SEQUENCE DESCRIPTION: (B) LOCATION 1...583
;
US-09-107-532A-5678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                 5-09-107-532A-5678
Sequence 5678, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
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                                                                                                                                                                     |: ::: :|||
463 PEQLNSLISVVFQD 476
                                                                                                                               179 FGVLSDVLTAIFQD 192
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Best Local Similarity 18.7%
Marches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCI
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Patent No. 6610836
GENERAL INFORMATION
APPLICANT: Gary Elecon et. al
APPLICANT: Gary Elecon et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE------VEFSVIPKSSGGL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 LIAAVAMIMRFAEPMAMFISYTSVVE----LIASALQRIERFWAIAPLPVAEQSEMPERY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VGIVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                               APPLICANT: SPECHT, THOMAS
APPLICANT: BLEAKALN, BERND
APPLICANT: HINZWANN, BERND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OP INTENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT APPLICATION NUMBER: US/09/673,395A
SOFTWAREN FILENG DAYS: 2000-10-17
NUMBER OF SEQ ID NOS: 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 VSAEKVNK---THSVNGITEBADPTIYSGKVIRPLRSVDPTQTEYQGMIBIVERGDMKGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 LAMRNIBARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHAD-KFERHVGIV---DFKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 84; DB 4; Length 410; 22.1%; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Mismatches
Sequence 197, Application US/09673395A
Patent No. 6620923
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CRGANISM: Klebsiella pneumoniae
US-09-489-039A-14142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.1<sup>§</sup>
Matches 40, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-673-395A-197
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US-09-489-039A-14142
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NAME/KEY: VARIANT
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                                                         164 TQMLFAHHGLTLRDKK--APSVFFVKKLKNTLNHVYGYAVL----SISSKQLANLFOSVV 217
135 IQDFVVALSLEISDEGNITMISFEVRQFANVVMHIGGLSILDPIFGVLSDVLTAIFQDTV 194
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                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.

PPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillion, Davin C.
APPLICANT: Ditter Probst
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
TITLE OF INVENTION: 1012.000-05-05
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Vorse, DENGTH: 845
TYPE: PPP
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CURRENT APPLICATION NUMBER: US/09/639,206A
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j OTHER INFORMATION: Xaa = Any Amino Acid
US-09-565-501A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : | | | | | 2 VNFTVDQVRELMDYPDQIRNMSVIAHVD-
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Leishmania major
                                                                                                                                                                                195 RKEMTKV 201
                                                                                                                                                                                                                                    |::|:
218 NPEISKI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT LOCATION: (1)...(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-09-639-206A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 DXRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 DANV----KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 EISDEGNITMTSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VNFTVDQVRELMDYPDQIRNMSVIAHVD------HGKSTLSDSLVGAAGIIKMEEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Cambos-Neto, Antonio
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Bratia, Rhea
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Tring of Invervion. Listanna, Mark
APPLICANT: Tring CP Invervion. Listanna, Mark
APPLICANT: Probst, Peter
APPLICANT: Samnon, Mark
APPLICANT: Set Invervion. Listanna, Autorion
APPLICANTON INVERSE: 10s/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 845
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.8%; Score 83; DB 4; Length 845; Best Local Similarity 23.3%; Pred. No. 2.1; Matches 42; Conservative 34; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 7.8%; Score 83; DB 4; Length 845; Best Local Similarity 23.3%; Pred. No. 2.1; Matches 42; Conservative 34; Mismatches 70; Indels
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 11.2
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 845
                                                                                                                                                                                                                                     FEATURE:
NAME/ERY:
LOCATION: (1)...(845)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-639-206A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(845)
CTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-110
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Patent No. 6638517
                                                                                                                                                                         TYPE: PRT ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Leishmania major
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269 MDYSAIPSVIFTHP-----EIAMVGLSLQEAEQQNLPAKLTKFPFKAIGKAVALGAS 320
212 AGVIRDDRGVIPVDETMRTNVPNIYAIGDIIGKWLLAHVASHQGVIAAKNISGHHB---V 268
                                                          114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMISFEVRO-
                                                                                                                                                                           162 --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                                                                                                                                                                                                   || :|:| : | : | : | : | 321 DGFAAIVSHEITQQILGAYVIGPHASSLIGEMTL----AIRNELT 361
                                                                                                                                                                                                                                                                                                                                                    US-08-461-722-2

US-08-461-722-2

Sequence 2, Application US/08461722

Patent No. 6335183

GENERAL INFORMATION:

APPLICANT: Young, Richard A. and Young, Douglas

TILE OF INVENTION: Stress Proteins and Uses Therefor

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.

STREET: 2 Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FILING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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PRICASSITICATION 18.435
PRICASTICATION NUMBER: PCT/US94/06362
PILING DATE: 06-UN-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
PILING DATE: 04-UM-1993
CLASSIFICATION: 435
PRICASSIFICATION: 435
PRICASSIFICATION: 435
PRICASSIFICATION: 435
PRICASSIFICATION NUMBER: US 07/86,581
PRICASSIFICATION NUMBER: US 07/366,581
PRICASSIFICATION NUMBER: US 07/207,298
PRICASSIFICATION NUMBER: US 07/207,298
PRICASSIFICATION NUMBER: B-UN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHI88-08AFA4
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02173
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STATE: M2
COUNTRY:
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Parent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REPRENCE: 9710-003-999

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ. ID NOS: 6849
                                                                                                                                                                                                Sequence 4657, Application US/09134001C

Parent No. 6380370

GENERAL INFORMATION:
APPLICANT: LAND NOUCE E-Stamm et al
APPLICANT: LAND NOUCE E-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: CO.07
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VGIV-DFKGELAMRNIEARGLKQMKRQCD-----ANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 MKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 SLEISDEGNITMISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AQOY -- HAHVITTDFNL---- NKVCHVQGITALN-----VNDLSEAIKPNVHQGDQLSIL 306
                                             EISDEGNITMISFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
7.7%; Score 82; DB 4; Length 362;
Best Local Similarity 24.4%; Pred. No. 0.74;
Matches 31; Conservative 27; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.7%; Score 82; DB 4; Length 397; Best Local Similarity 20.4%; Pred. No. 0.85; Matches 46; Conservative 44; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 APAFKRE 209
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                                                                                                                                                            RESULT 20
US-09-134-001C-4057
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US-09-198-452A-894
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72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
                                                                                                                                                                                                                                                                                                                                                                                                                157 TVGKLIABAMDKV-----GKBGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------EGNITMTSFEVRQ 161
                                                                                                                                                                                                                                                                         13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 PETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 FANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||: :: ||||
263 ---VVNTIRĠIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEBIGMELEK 311
                                                                                                                                                                        7.6%; Score 81.5; DB 4; Length 547;
20.4%; Pred. No. 1.6;
tive 37; Mismatches 85; Indels 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-468-041-2

| Sequence 2: Application US/09468041
| Patent No. 6482614
| GENERAL INFORMATION:
| TITLE OF INVENTION:
| TITLE OF INVENTION: Stress Proteins and Uses Therefor INVENTE OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. |
| STREET: 2 Militia Drive | STATE: MA
| STATE: MA
| STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRATION TAPLICATION DATA:
APPLICATION NUMBER: US/09/468,041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 PITHVISDIQDFVVALSLEISD--------
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APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-UN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-UN-1989
ATTORNEY/AGENT INPORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-UNN-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
                                 547 amino acids
                                                                                                                                                                                                 Best Local Similarity 20.49
Matches 48; Conservative
                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                       US-08-336-251-2
                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                    ----EGNITMTSFEVRQ 161
                                                                                                                  13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                162 FANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                               263 ---VVNTIRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEEIGMELEK 311
                              DB 4; Length 547;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Young, Richard S,
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
                      7.6%; Score 81.5; D 20.4%; Pred. No. 1.6; Live 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-NOV 1994
CLASSIFICATION: 435
PRIOR APPLICATION 1935
PRIOR APPLICATION: 435
FLING DATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 09-DEC-1991
FILING DATE: 09-DEC-1991
FILING DATE: 10-JUN-1993
FILING DATE: 15-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: WHI88-08AFA3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  PTTHVISDIQDFVVALSLEISD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-336-251-2
; Sequence 2, Application US/08336251
; Patent No. 6338952
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REGISTRATION NUMBER: 32,227
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ATTORNEY/AGENT INFORMATION:
Query Match
Best Local Similarity 20.4%,
-has 48; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-UNN-1994
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA2 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         Query Match 7.6%; Score 81.5; DE Best Local Similarity 20.4%; Pred. No. 1.6; Matches 48; Conservative 37; Mismatches
REGISTRATION NUMBER: 32,227
REFREEMCE/POCKET NUMBER: WHI88-08AFA3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-UTN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 PTTHVISDIQDFVVALSLEISD----
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                                                                      | INFORMATION FOR SEQ ID NO. SEQUENCE CHRACTERISTICS. SEQUENCE CHRACTERISTICS. TYPE: amino acid TYPE: amino acid TYPE: amino acid MCCOLGY: linear MCLCCULE TYPE: protein US-09-468-041-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 861-6240 INFORMATION FOR SEQ ID NO: 2:
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amino acid
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MOLECULE TYPE: protein
PCT-US94-06362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SE:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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PCT-US94-06362-2
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APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Saucrbaum, Sebastien
APPLICANT: Saucrbaum, Sebastien
APPLICANT: Saucrbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                          72 AMRNIEARGLKQMKRQGDANVKGEEGIVKAHILIGVHDD---IVSMEYDLAYKLGDL--H 126
                                                                                                                                                                                                                                                                                                       157 TVGKLIÅEAMDKV------GKEGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINK 207
                                                                                                                                                                                                                                                                                                                                                                     127 PTTHVISDIQDFVVALSLEISD---------EGNITMISFEVRQ 161
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                                                                                                                          13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
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                                                                65;
Query Match 7.6%; Score 81.5; DB 5; Length 547; Best Local Similarity 20.4%; Pred. No. 1.6; Matches 48; Conservative 37; Mismatches 85; Indels 65
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
PRIOR APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
ATCHARRY/AGRYT INFORMATION:
NAME: MAYERS. KENDECH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03495.0137-02000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFRENCE/DOCKET NUMBER: 03495
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1300 I Street, N.W.
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
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127 PTTHVISDIQDFVVALSLEISD----
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n, Sebastien
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amino acid
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Best Local Similarity
Matches 48; Conserv
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STREET: 13
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                                                                                                                                                                                                                                                                                                                                                                      ---VNNTIRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEEIGMELEK 311
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                                                                     Length 548;
                                                                                                       85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SOGO, Kazuyo
APPLICANT: SOGO, Kazuyo
APPLICANT: YANGI, Hideki
APPLICANT: YANGI, Hideki
APPLICANT: YARAGI,
TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REPERENCE: 1422-409P
CURRENT PILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: JP10-372965
EARLIER PILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 7
                                                                     DB 2;
                                                                  7.6%; Score 81.5; Di
20.4%; Pred. No. 1.6;
tive 37; Mismatches
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Patent No. 6248330
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09472971
Patent No. 6197547
GENERAL INFORMATION:
                                                                    Query Match
Best Local Similarity 20.4%
Matches 48; Conservative
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SEQ ID NO 3
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US-09-472-971-3
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-467-822-32
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Best Local Similarity
Matches 48; Conserv
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US-08-432-697-32
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US-09-472-971-3
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS ACAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 VAAGWNPM------DLKRGIDKAVTAAVE----LKALSVPCSDSKAIAQVGTISANSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 548;
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Sequence 32, Application US/08466248
Patent No. 6258359
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 2005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                               Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mayers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO. 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 81.5; DE 20.4%; Pred. No. 1.6; Live 37; Mismatches
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44;

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59 BRHVGIVDFKGELAMRNIE--ARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 -----ALAIQAIKLIANNLRQAVALGE-NLEARENWAYASLLAGMAFNNANLGY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 --DLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNIIMTSFEVRQFANVVNHIG---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 VHAMAHQLGGLYDMAHGVAN-----AMLLPHVERYNLISNP---KKFADIAEFMGENIE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MKFLLIAAVAFVAVSA-DPIHYDKITEEINKA--IDDAIAAIEQSETIDPMKVPDHADKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                               71; Indels
                APPLICANT: Selifonova, Olga V.
TITLE OF INVENTION: Mutant 1,3-Propanediol Dehydrogenase
FILE REFERENCE: GCON.
CURRENT APPLICATION NUMBER: US/09/570,778A
CURRENT FILING DATE: 2000-05-14
PRIOR APPLICATION WUMBER: US 60/134,868
PRIOR PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 81; DB 4
23.8%; Pred. No. 1.1;
tive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 GLSI-----LDPIFGVLSDV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 GLŚVMEAAEKAIDAMFRLSKDV 336
                                                                                                                                                                                                                                                           TYPE: PRT CORGANISM: Clostridium pasteurianum US-09-570-778A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Clostridium pasteurianum
                                                                                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 AMRNIBARGLKOMKROGDANVKGBEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | : : | : : | 1111: | 127 TVGKLIABAMDKV------GKEGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PITHVISDIQDFVVALSLEISD-----EGNITMISFEVRQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 FANVANHIGGL----SILDPIFGVLSDVLTAIPQDTVRKEMTKVLAPAFKRELEK 212
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                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-315
ZUNDUM TYBE: FLODBY disk
MEDIUM TYPE: FLODBY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION HASE: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION WASER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION WASER: US 08/495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEDRONE: (202) 408-4400
TELECOMMUNICATION INFORMATION:
TELEDRONE: (202) 408-4400
INFORMATION FOR SEO ID NO: 32:
SEQUENCE CHARACTERISTICS:
LEXGTH: AMINO acids
TUDE: AMINO acids
                                                                                                                      ADDRESSE: Tinnegan, Henderson, Farabow, Garrett ADDRESSE: Dunner STREET: 1300 I Street, N.W. CITY. Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
             TITLE OF INVENTION: HELL TITLE OF INVENTION: COME INTLE OF INVENTION: POLY NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Conservative
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MOLECULE TYPE: protein
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Best Local Similarity
Matches 48; Conserva
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216 ------ALAIQAIKLIANNIRQAVALGE-NIEARENMAYASILAGMAFNNANIGY 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 ERHVGIVDFKGELAMRNIE--ARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEY
Sequence 12, Application US/0999138
Fatent No. 655893
GENERAL INFORMATION:
APPLICANT: Trimbur, Donald E.
APPLICANT: Trimbur, Donald E.
APPLICANT: Whited, Gregory M.
TITLE OF INVENTION: Mutant I, 3-Propanediol Dehydrogenase
FILE REFERENCE: GC580-2D1
CURRENT APPLICATION NUMBER: US/09/991,138
CURRENT APPLICATION NUMBER: US 09/570,778
PRIOR APPLICATION NUMBER: US 09/570,778
PRIOR PLING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FateSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 81; DB 4; Length 385;
23.8%; Pred. No. 1.1;
tive 39; Mismatches 71; Indels
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; Sequence 12, Application US/09570778A; Patent No. 6468773; GENERAL INFORMATION: APPLICANT: Trimbur, Donald E.; APPLICANT: Whited, Gregory M.

RESULT 30 US-09-570-778A-12

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Sequence 8512, Application US/09489039A
Sequence 8512, Application US/09489039A
Patent NO. 6610836
GENERAL INFORMATION:
APPLICANT GATY Breton et. al
TILLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TILLE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 DDIVSMEYDLA-YK-----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 NDKLVYRMDAEDFKKCLDINLIGTFNWTQHVLKKWMKQREGAIINLSSVSGLIGNIGQAN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VKGEEGIVKAHLLI---GVH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 FEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 YAASK-AGVVGLIKSVAREAATRGIICNAIAPGF---IITDMIEVLADKVKEQAEK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.5%; Score 80.5; DB 4; Best Local Similarity 18.1%; Pred. No. 1.2; Matches 43; Conservative 43; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.5%; Score 80.5; DB Best Local Similarity 23.3%; Pred. No. 0.64; Matches 41; Conservative 35; Mismatches
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: 1017 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ALTHORMATION:
REPERBONG/DOCKET NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REPERBONG/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-5007
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 IVDFKGEL---AMRNIEARGLKOMKROGDAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...255
; SEQUENCE DESCRIPTION: SEQ ID NO: 4950:
US-09-107-532A-4950
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                              LENGTH: 255 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-489-039A-8512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                            APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, ARMIN
APPLICANT: SCHWITT, ARMIN
APPLICANT: SCHWITT, ARMIN
APPLICANT: PLARSKY, CRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHAD-KFERHVGIV---DFKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 LAMRNIBARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 81; DB 4; Length 470; 22.9%; Pred. No. 1.4; tive 29; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 -----YKLGDLHPTTHVISDIQDFVVALSLEISDE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
COMPUTER: PC
COMPANDS SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4950, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                171 GLSI-----LDPIFGVLSDV 185
                                                                                                           |||: :| : ||
315 GLSVMEAAEKAIDAMFRLSKDV 336
                                                                                                                                                                                                                                           Sequence 561, Application US/09673395A Patent No. 6620923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-09-673-395A-561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02354
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                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -532A-4950
                                                                                                                                                                                                   RESULT 32
US-09-673-395A-561
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31; Gaps

Indels

Length 374;

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421 LLAALAHAAIGA-----AGEDLRQVVGEPADVVRDRHVV---VVEDH-----QHVG-V 464
                                                                                                                                                                                                                                                                                                                                               100 ------KAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEI 146
                                                                                                                                                                                                                                                                                                                                                                               525 AAREGRQAVLLAQGAHQLAALGEDLV-----RIG-----LVADVPDQAVVRSVED 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 -----SLEISDEGNITMTSFEVRQ-FANVVNHIG------GLSILDPIFGVLSD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 DFKGEL-----EEGIV---- 99
                                                                                                                                                                                                                                                                                                      465 DFRGVVECLEGHAGGQRTVADHGHRLTLLALQAGGDGHAQGGADGGAGVADAEGVVLALC
                                                                                                                                                                 6 LIAAVAFVAVSADPIHYDKITEBINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 LOESINOALDHVRDAEDMNRAI-TFKQRDHEKQHERVKEQMEVVGASLSMSADSLTIPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ITBEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQM
                                                                                                                           70;
                                                                             DB 4; Length 1504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 80; DB 4; Length 1792;
21.3%; Pred. No. 14;
ive 39; Mismatches 90; Indels
                                                                                                                           46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tryggvason, Karl
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REFERENCE: 99,274-D
CURRENT APPLICATION WYBER: US/09/561,818A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REFERENCE: 99,274-D
                                                                        Query Match
7.5%; Score 80; DB 4
Best Local Similarity 21.1%; Pred. No. 11;
Matches 39; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 IDTQIIYH--KDESDNLLNQA--RELQ 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-561-818A-12
Sequence 12, Application US/09561818A
Sequence 12, Application US/09561818A
PERENT No. 6638907
GENERAL INPORMATION:
APPLICANT: Kortesmaa, Jarrko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS-09-561-818A-10
Sequence 10, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
APPLICANT: Kortesmaa, Jarrko
       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 44; Conserve
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LENGTH: 1792
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Best Local S:
Matches 44
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Sequence 26608, Application US/09252991A

Patent No. 6551795

GENERATION: MARC J. Rubenfield et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MERCALION PRERIODED

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

LENGTH: 1504

TYPE: PRI
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 538
                                                ---KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
                                                                               212 PDTGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLVIIAEDVEGEALATL---- 266
---GKEGVITVEDGTGLEDELDVVEGMQFDRGYLSPYFINK 211
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                                                                                                                                                             Gaps
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                                                                                                                                    160 RQFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK
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21.6%; Pred. No. 2;
cive 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-19476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Conservative
  161 TVGKLIAEAMDKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 44; Conserv
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US-09-252-991A-26608
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APPLICANT: Parting, Matthew W.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: ISOLATION OF AN MC 52,000 FK506 BINDING HUMAN
TITLE OF INVENTION: ODNA
TOTHER OF INVENTION: CDNA
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 QQEADELSRNIHSSDWNGLVQKALDASNVYENIANYVSEANETAELALNITDRIYDAVSG 650
                                                                                                                                                                                                                                                                                                                   85 K-RQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTH-VISDIQDFVVAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 -----SLEISDEGNITMTSFEVRQ-FANVVNHIG-----GLSILDPIFGVLSD 184
                                                                                                                                                                                                                                                                                       25 ITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQM
                                                                                                                                                                                                                                                                                                                                                                                                 540 TLEELDEIIKNASGI------YAEIDGAKNELQGKLSNLSNLSHDLVQEATDHAYNL
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                        DB 4; Length 1816;
                                                                                                                                                                                                                                                    90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive
CITY: Carbington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                          Query Match
7.5%; Score 80; DB 4
Best Local Similarity 21.3%; Pred. No. 15;
Matches 44; Conservative 39; Mismatches
CURRENT APPLICATION NUMBER: US/09/561,818A CURRENT FILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDTQIIYH--KDESDNLLNQA--RELQ 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VLTAIFQDTVRKEMTKVLAPAFKRELE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPI91-06A
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APPLICATION NUMBER: 07/963,325
FILING DATE: 16-007-1992
APPLICATION NUMBER: US 07/777,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08336618 Patent No. 5763590 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VPJ
TELECOMMUNICATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                          TYPE: PRT
CRGANISM: Mus musculus
US-09-561-818A-10
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                                                                                                          LENGTH: 1816
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Sequence 6606, Application US/09543681A

Sequence 6606, Application US/09543681A

Sequence 6606, Application US/09543681A

Sequence 6606, Application US/09543681A

GREERT NO. 660570.

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL1

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REPERBENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                            63 GIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKL 122
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                                                                                                                                                                                                                                                                                 ---DPMKVPDHAD-KFERHV
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                                                                                                                                                                                7.4%; Score 79.5; DB 1; Length 458; 22.1%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 557;
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                                                                                                                                                                                                                                       29; Mismatches
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US-08-094-889-1
i Sequence 1, Application US/08094889
Patent No. 5470966
GENERAL INFORMATION:
APPLICANT: Shinji HIRANO et al.
                       Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 17.7%
Matches 42; Conservative
                                                                                                                                                                                              Ouery Match
Best Local Similarity 22.1%
Matches 27; Conservative
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acidi
                                                                                                                          , MOLECULE TYPE: protein US-08-336-618-24
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us-10-024-955-7.rai

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RESULT 42

US-09-522-991A-27391

i Sequence 27391, Application US/09252991A

i Patent No. 6551795

i GENERAL INFORMATION:

i TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR PAPLICATION NUMBER: US 60/074,190

PRIOR PAPLICATION NUMBER: US 60/094,190

                                                                                                        10;
                                                                                                                                                                                            361 DPLNIAIDKMTKKTRDLRRQLRKAVMDHISDSFLETNVPLLVLIBAAKSGNEKEVKEYAQ 420
                                                                                                                                                                                                                                                                                     88 GDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEIS 147
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                                                                                                                                                    18 DPIH--YDKITE-----EINKAIDDAIA------AIEQSETIDPMKVPDHAD 56
                                                                                                         71; Gaps
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                                             Query Match 7.4%; Score 79.5; DB 1; Length 906; Best Local Similarity 19.4%; Pred. No. 5.8; Matches 48; Conservative 47; Mismatches 82; Indels 7:
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7.4%; Score 79; DB 4; Length 400;
Best Local Similarity 20.4%; Pred. No. 1.9;
Matches 43; Conservative 46; Mismatches 74; Indels
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                                                                                                                                                                                                                                                     57 KFERHVG-IVDFKGELAMRNIBARGLKQMK-----
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US-09-252-991A-32411
; Sequence 32411, Application US/09252991A
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584 PRFAEQVE 591
US-08-094-889-1
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Sequence 6150, Application US/09134000C
Sequence 61510, Application US/09134000C
Sequence 61716
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BATEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNCE: 032796-032
CURRENT PILITING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,000C
GURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1999-08-15
                                                                          Sequence 3522, Application US/09134000C

Betent No. 6647156
GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETCE-STAMM et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 02796-03
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
RRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PETENTIN VETSION 3.1
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 21.7%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative
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Best Local Similarity
Matches 54; Conserv
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US-09-134-000C-6150
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LENGTH: 437
TYPE: PRT
ORGANISM: EDE
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APPLICANT:
MARC J. RUBERFIEL ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23008
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ENGITH: 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AAIEQSETIDPMKVPD-----HADKFERHV-GIVDFKGELAMRNIEARGLKQMKRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%; Score 79; DB 4; Length 593; 23.6%; Pred. No. 3.5; Live 25; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AVVQLAEHTEVLLRVVEGRQPAQVQCLVGAGAGVVDP 201
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; Patent No. 6551795
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US-09-252-991A-23008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
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GOS VGKTELARALAESMEGDDDAMIRVDWSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 462
                                                                   121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 DTLHERVIGOXDAVNSISKAVRRARAGLK----DP-----KRPIGSFIFLGPTG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 MRNIB-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV------HDDIVSMEYDLAY 120
                                                                                               | : :: | | : :: | 463 K----PYSVILFDEIBKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIMTSNVGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 DPIHYDKITEE-----INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                  173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                        518 ELODORFAGFGGSSDGODYETIRKTMLKELKNSFRPE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 78.5; Di 22.6%; Pred. No. 4.8; tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-0x11-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/040,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
RADDRESSEE: Dechert, Price & STREET: 4000 Bell Atlantic CITY: Philadelphia
                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09621855
Patent No. 6346608
GENERAL INFORMATION:
APPLICANT: Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                        Wang, Min
Shilling, Lisa K.
Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hodgson, John E.
Lawlor, Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Fosberry, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ward, Judith
TITLE OF INVENTION: MecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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Matches 49; Conserva
                                                                                                                                                                                                                                                                      US-09-621-855-4
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                                    ----FRIQRQVNSIIKEEBYLALQHL-----TRTRYQ 170
                                                                                                                                                                                      64 -----IVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
                                                                                                            161 OFANVVNHIGGLSILDP--IFGVLSDVLTA-----IFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRNIE-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 DPIHYDKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
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                                                                              LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: windows 95
SOFTWARE: FRSEESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
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7.4%; Score 78.5;
Best Local Similarity 22.6%; Pred. No. 4.
Matches 49; Conservative 37; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: 3710082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GM10082
                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09040843
Patent No. 6124119
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Jaworski, Deborah J.
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Shilling, Lisa K.
Burnham, Martin
Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: MeCB
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTER: IBM COMPALIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 672 amino acids
amino acid
                                        133 QIDAFYIADY-----
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                                                                                                                                                                                                                                                            RESULT 47
US-09-040-843-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                        121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMISFEVRQFANVV----NHIGGL 172
                                                                                                                        18 DPIHYDKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
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549 VGKTELARALAESMFGDDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-011-2000
CLASSIFICATION: <university of the company of the c
                                                                                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 DILHERVIGOKDAVNSISKAVRRARAGLK----DP-
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/040,843
FILING DATE: <unimormal control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 866 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09621855
Patent No. 6346608
GENERAL INFORMATION:
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Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lisa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
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Best Local Similarity 22.6%
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, Min
Shilling,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 50
US-09-621-855-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 DTLHERVIGGKDAVNSİSKAVRARAĞLK----DP------KRPIĞSPIFLĞPTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 DPIHYDKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                        121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNIIMTSFEVRQFANVV----NHIGGL 172
                                                                                                                                                                                    463 K----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIIMTSNVGAQ S17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                 173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows 95
SOFTWARE: FRANCED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
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7.4%; Score 78.5; Di
Best Local Similarity 22.6%; Pred. No. 7;
Matches 49; Conservative 37; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/DEMT INFORMATION:
RAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GM10082
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Patent No. 6124119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jaworski, Deborah J.
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TELEPHONE: 215-994-2488
TELEFAX: 215-994-222
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Shilling, Lisa K.
Burnham, Martin
Fosberry, Andrew
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Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
COMPUTER: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 866 amino acids
amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hodgson,
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; TOPOLOGY: linear
US-09-040-843-2
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TITLE OF IN
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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70 E-----EGIVKAHLLIGVHDDIVSM 114
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                                                                                                                                                                                                                                                                                                                                                        115 EYDLA--YKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMISFEVROFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                           ----AADTG-----LORAEAVAHAPGV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHARLO INFECTIONS EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THERRON
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                               13 VAVSADPIHYDKITE--EINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIV-DFKG 69
                                                                                64;
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                    Query Match
7.3%; Score 78; DB 4; Length 516;
Best Local Similarity 25.1%; Pred. No. 3.6;
Matches 49; Conservative 27; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 11755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUREALING SISIENT FC-LOOF/AS-LOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/219,262B

FILING DATE: 29-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 2747-047-27

TELEPHONE: (703) 413-220

TELECAMONICATION INFORMATION:

TELECAMONICATION INFORMATION:

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TELECAMONICATION INFORMATION:

TELECAMONICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 1012 amino acids
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08219262B Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                 225 RLDOAAHHRVGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 SI-LDPIFGVLSDVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 DLALEEIDQVVGDGL 269
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Best Local Similarity
Matches 39; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 53
US-08-219-262B-7
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
FRICR APPLICATION NUMBER: US 60/074,788
FRICR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19045
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
NUMBERNOE:
2709.200400.1
CURRENT APPLICATION NUMBER: US /09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 MRNIEARGLKOMKROGDANVKG-----EEGIVKAHLLIGVHD---DIVSMEYDL----A 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 YKLGDLHPTT-HVISDI------QDFVVALSL------EISDEGNITMTSFE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 HEFSDVLPTAYHSIIDVLSKPEQKVEHEQLSLLFSLMIYHDLRKQGKVDDEINI----- 186
                                                     121 KLGDLHPITHVISD----IQDFVVALSLEISDEGNITMISFEVROFANVV----NHIGGL 172
                                                                                                           609 K-----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIMTSNVGAQ 663
549 VGKTELARALAESMFGDDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 DPIHGTIRLTTLEIASINHPLEQRIRNIKQNSFLYKVFPSAVHSRFEHSLGVLHLSSEL- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 DPIHYD-KIT----EEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.3%; Score 78; DB 4; Length 511; Best Local Similarity 21.2%; Pred. No. 3.6; Matches 45; Conservative 38; Mismatches 75; Indels
                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                      664 ELQDQRFAGFGGSSDGQDYETIRKTMLKELKNSFRPE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 VRQFANVVNHI ----GGLSILDPIFGVLSDVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 ----ENVLKIIEKRYGDQQIIEEINGKATDIL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19045, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                     Sequence 7682, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-19045
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                                                                                                                                                                                                                                                                                                      RESULT 51
US-09-489-039A-7682
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Sequence 7, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
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(703) 413-2220
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 39, Conserve
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; STRAIN: 52/70
US-09-031-655-7
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                                                                99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                      157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPRMVATCDSSDRPRVYTI 208
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APPLICANT: SNYDER, DAVID B
APPLICANT: MYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMBELIC INPECTIOUS BURSAL DISBASE VIRUS
TITLE OF INVENTION: CHIMBELON
TITLE OF INVENTION: THERRON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI 98
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: OBLOM, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMINICATION INDERNATION:
TELECOMMINICATION INDERNATION:
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Patent No. 5788970
GENERAL INFORMATION:
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TELEFAX: (703) 413-220
TELEX: 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
TYPE: amino acids
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Best Local Similarity 23.2.
Local 39; Conservative
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US-08-219-262B-8
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102 VSRSITVRSSTLPGGVYALNGTINAVTPQGSLSELTDVSYNGL----MSATANINDKIG- 156
                                                                                                                                                                                                                                                                                                                 APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: SNYDER, DAYLD B
APPLICANT: STILL SOFT STATE
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 IEQSETIDPMKVPDHADKFERHVGIVDRKGELA-MRNIEARGLKOMKRQGDANVKGEEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Gaps
155 TSPEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                          209 TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSVGGELVFQTSVQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSIGGELVFQTSVQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.3%; Score 78; DB 3; Length 1012; illarity 23.2%; Pred. No. 10; Conservative 37; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 APPLICATION NUMBER: US/09/031,655 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 2747-047-27
TELEPHONE: (703) 413-3000
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Sequence 31003, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. 6551703
PPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ADMINO ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
                        APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 GELAMR-NIEARGLKQMKRQCDANVKGEEGIVKAHLL-----IGVHDDIVSMEYDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 -----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTSFEVROFANVVNHI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 QPNKEHMDMPSLHSLEHLTAELIRNHADYIV----DWSPMG--COTGF----YLTVLMHE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 77.5; DB 4; Length 166; 25.9%; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: D/NOW 1203000
COMPUTER: PC
OPERATING SYSTEM: <UNKnown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILLING DATE: 30-7un-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILLING DATE: UNLY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...166
SEQUENCE DESCRIPTION: SEQ ID NO: 5004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGHED SOURCE:
ORGANISM: Enterococus faecium
                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 SYEDILDVLEATMKDVLEA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 GGLSILDPIFGVLSDVLTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (761)893-8277
INFORMATION FOR SEQ ID NO: 5004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.99
Matches 36; Conservative
                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                           COUNTRY: USA
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 58
US-09-252-991A-31003
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                                                              Sequence 8, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
APPLICANT: VACHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MINCEL-WHERSAY, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IEQSETIDPMKVPDHADKFERHVGIVDFKGBLA-MRNIEARGLKOMKROGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 TSFEVROFANVANHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::||::||::||:|
209 TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSVGGELVFQTSVQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 78; DB 3; Length 1012; 23.2%; Pred. No. 10; ve 37; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                   S: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Infectious bursal disease virus STRAIN: STC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 277-047-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPHONE: (703) 413-320
TELERA: (703) 413-220
TELERA: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 57
US-09-107-532A-5004
; Sequence 5004, Application US/09107532A
; Patent No. 6583275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-09-031-655-8
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361 DLFQLQKHRLQIAKRYIEKIQPSGGTNI--NEALLRAIFILNEANNLGLLDPNSVSLIIL 418
                                                                                                                                                                                                                                                                                                                                                                                                          479 N-QDTSSQLKKFYNQVSTPLLRNVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGKFDPAK 537
                                                                                                                                                                                                                                                                                          76 -----IEARGLKOMKRQGDANVKGEEGIVKAHLLIGVHDDIVSME---YDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DPI- 178
                                                                                                                                                                                                         19 PIHYDKITEEINKAID--DAIAAIEQSETIDPWKVPDHADKFERHVGIVDFKGEL-AMRN 75
                                                                                                                                                                   Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 FGVLSDVLTAI-------FQDTVRKEMTKVLAPAFKREL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |:|| | | || |:|| s38 LDQIESVITATSANTQLVLETLAQMDDLQDFLSKD--KHADPDFTRKL 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Batterson, Chandra
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                      84;
                                                                                                                                                                                                                                                                                                                                                                                  122 LGDLHPTT-----HVISDIQDFVVALSL
                                                                                                                      Query Match
7.3%; Score 77.5; DB
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: WORD Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,774
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0505 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09388774 Patent No. 6228991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUEDUCE CHARACTERISTICS: LENGTH: 946 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                    IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: gi33985
US-09-074-579-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 60
US-09-388-774-3
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134 EKAAAKINQALDECLSA--HMMTPRPGSLPALPPAFDRDEPRRPSTHAPGLLDKMLLRSS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 KGELAMRNIEA---RGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGD 124
                                                                                                                                                                                                                                                                                                                                                                23 DKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER-----HV-GIVD-----F 67
                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                           Query Match 7.3%; Score 77.5; DB 4; Length 409; Best Local Similarity 24.2%; Pred. No. 2.9; Matches 40; Conservative 28; Mismatches 62; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 L------HPTTHVISDIQDFVVALSLEISDEGNITMTSFEVR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09074579
Patent No. 6001596
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31003
LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0505 US
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APPLICATION NUMBER: US/09/074,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 946 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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APPLICANT: Teem, John L.
TITLE OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy
FILE REFERENCE: FSU-99XCII
CURRENT APPLICATION NUMBER: US/09/425,453A
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,444
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy TITLE OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy FILE REFERENCE: FSU-99XC1 CURRENT APPLICATION NUMBER: US/09/425,453A CURRENT FILING DATE: 1999-10-22 PRIOR APPLICATION NUMBER: 60/105,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 GIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 FEVRQ--FANVVNHIGGLSILDPIFGVLSDVLT--AIFQDTVRKEM---TKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 GOMARISLÁRAVYKDADLYLLDSPFGYL-DVLTEKBIFESCVCKLMANKTRILVTSKMEH 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 GIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 GTIKENIIFGV-----SYD-EYRYRSVIKACQLEEDISKFAEKDNM-VLGEGGITLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%; Score 77.5; DB 4; Length 1480; Best Local Similarity 28.5%; Pred. No. 21; Matches 35; Conservative 21; Mismatches 50; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.3%; Score 77.5; Dest Local Similarity 28.5%; Pred. No. 21; Mismatches 35; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 63
US-09-425-453A-18
; Sequence 18, Application US/09425453A
; Patent No. 6468793
; GENERAL INFORMATION:
          Sequence 8, Application US/09425453A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 1480
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-425-453A-18
                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1480)
US-09-425-453A-8
                                 Patent No. 6468793
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          LENGTH: 1480
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Patent No. 6562958
GENERAL INFORMATION:
FALLEL INFORMATION:
FILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                 | : | | : | | : | | : | | : | | 301 PDNLDPIPKNILFVIDVSGSMWGVRMKQTVEAMKTILDDLRAEDHFSVIDFNQNIRTWRN 360
                                                                                                                                                                                                                                                                                                                                                                   -----IEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSME---YDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                                                  419 VSDGDPTVGELKLSKIQKNVKENIQDNISLFSLGMGFDVDYDFLKRLSNENHGIAQRIYG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DPI- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSME--YDLAYKLGDLHPTTH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 FRNISFDELK------ENYIEATHALIEGGADIILIETVFDTINCKAAIFAVKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 VISDI-QDFVVALSLEISDEGNITMTSFEVRQFANVVNH-----IG-----GLSILDPIF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 VFKQIGRELPIMISGTITDASGRILTGQTAEAFWNSVRHGDLLSIGFNCALGADAMRPHV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 N-QDTSSQLKKFYNQVSTPLLRNVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGKFDPAK 537
                                                                                                                                                                                                                                                                  19 PIHYDKITEEINKAID--DAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL-AMRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 VSMSDYHMEDLVPEINREAARLAKAACEKYSTPDKPRFVAGVLGPTSRTCSISPDVNNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 VSADPIHYDKITEEINK-AIDDAIAAIEQSETID-PMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                    84; Indels 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FODTVRKEMTKVLAPAFKREL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 LDQIESVITATSANTQLVLETLAQMDDLQDFLSKD--KHADPDFTRKL 583
                                                                                                                                                                           Length 946;
                                                                                                                                                                        DB 3;
                                                                                                                                                                   Query Match
7.3%; Score 77.5; Di
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 LGDLHPTT------HVISDIQDFVVALSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 NITMTSFEVRQFANVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Acinetobacter baumannii
US-09-328-352-5704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 FGVLSDVLTAI------
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIERARY: GENEBANK
; CLONE: gi33985
US-09-388-774-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 50; Conserval
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US-09-328-352-5704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 62
US-09-425-453A-8
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ORGANISM:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL----DPKWATCDSSDRPRVYTI 208
                                                                                                                                APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, MERNAT, STEPHANIE A
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THERBON
NUMBER OF SEQUENCES: 15
CORRESPONDENCES ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: : ||: : ||: | | :| | :| TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSVGGELVFQTSV 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 77; DB 1; Length 1012; Best Local Similarity 23.4%; Pred. No. 13; Matches 39; Conservative 36; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON, PRIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F 24,618
REGISTRATION NUMBER: 2747-047-27
TELEPROMOJICATION INFORMATION:
TELEPROMOJICATION INFORMATION:
TELEPROMOJICATION INFORMATION:
TELEPRAK: (703) 413-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Infectious bursal disease virus ; STRAIN: E/DEL US-08-219-262B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 65
US-08-219-262B-5
; Sequence 5, Application US/08219262B
; Patent No. 2788970
GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
                                                              Sequence 3, Application US/08219262B Patent No. 5788970 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENGTH: 1012 anino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                -08-219-262B-3
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MENGEL-WHERSAT, STEPHANIE A
VENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
VENTION: CHIME CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
VENTION: THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
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US-08-541A-30
Sequence 30, Application US/08708541A
Patent No. 5871744
GENERAL INFORMATION:
APPLICANT: VAKHARIA, Vikram N.
APPLICANT: WAKHARIA, Vikram N.
TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
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                               TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE V.
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP 655 Fifteenth Street, N. W., Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARES PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B FILING DATE: 29-MAR-1994
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN P
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 27,419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Infectious bursal disease virus CU-1
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.4%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
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STREET:
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FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.4 Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Inf
STRAIN: E/DEL
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-031-655-3
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Sequence 3, Application US/09031655

Parent No. 6017759

GENERAL INFORMATION:

APPLICANT: VAKHARIA, VIKRAM

APPLICANT: VAKHARIA, VIKRAM

APPLICANT: WAYDER, DAYID B

APPLICANT: MENGEL-WHERSAT STEPHANIE A

TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS

TITLE OF INVENTION: THEREON

TITLE OF INVENTION: THEREON

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON

STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL----DPKMVATCDSSDRPRVYTI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 ISFEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 77; DB 2; Length 1012; 23.4%; Pred. No. 13;
                                 CUUTATE: U.C.

ZIP: 2005-5701

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/708,541A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONIGA C.
REGISTRATION NUMBER: 36.105
REFERENCE/DOCKET NUMBER: P8172-6002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1012 amino acids
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TOPOLOGY: linear
Washington
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COUNTRY: USA
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-708-541A-30
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99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
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209 TAADDVQFSSQYQP-GGVTI--TLFSANIDAITSLSVGGELVFQTSV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 77; DB 3; Length 1012; 23.4%; Pred. No. 13; 64; Indels iive 36; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIENTINA COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Infectious bursal disease virus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
                 US 08/219,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: US/09/031,655 FILING DATE:
PRIOR AFFILLAND NUMBER: US 08/219,
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAR: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-
TELECOMMUNICATION INFORMATION:
TELEPHAN: (703) 413-220
TELEPHAN: (703) 413-220
TELEPHAN: (703) 413-220
TELEPHAN: (703) 413-220
TELEPHAN: (703) 413-220
TELEPHAN: (703) 413-220
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TELEPHAN: (703) 413-220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: P-LOS/MS-
SOFTWARE: Patentin Release #
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ORGANISM: Enterococcus faecium
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US-09-107-532A-3785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                      7.2%; Score,77; DB 3; Length 1012; 23.4%; Pred. No. 13; tive 36; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERATING BIRNAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09147711
Patent No. 6596280
GENERAL INFORMATION:
APPLICANT: WORDER, VIKERM N.
APPLICANT: MUNDT, Egbert
TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVI
TITLE OF INVENTION: FROM SYNTHETIC RNA TRANSCRIPTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/147,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: ARENT FOX KINTNER PLOTKIN & KAHN STREET: 1050 Connecticut Ave., N.W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 31-JUL-97
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/708,541
FILING DATE: 05-SEP-96
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MOMILGE C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 9108288-09002
REGISTRATION NUMBER: 24,618
REFERRNCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-200
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
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STEANDENDERS:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/198,913
APPLICATION NUMBER: 24-NOV-98
PUTTY DATE: 24-NOV-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTRY: USA
ZIP: 20036-5339
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 23.49
                                                                                                                                                                                                                                                                                                          ORGANISM: Int
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US-09-147-771-30
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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Sequence 3785, Application US/09107532A
Sequence 3785, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|:| ::|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Score 77; DB 4; Length 1012; Best Local Similarity 23.4%; Pred. No. 13; Matches 39; Conservative 36; Mismatches 64; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PC
COMPUTER: PC
COMPAGE: ACII
SOFTWARE: ACII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,798
APPLICATION NUMBER: 60/085,798
APPLICATION NUMBER: 2,1997
ATTORNEY/AGENT: INFORMATION:
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REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 429 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (781)893-8277
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SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION: TELEPHONE: 202/857-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                      : 1012 amino acids
amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                           TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...164;
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SEQUENCE DESCRIPTION: SEQ ID NO: 6514:
US-09-107-532A-6514
                                                                                              Query Match
Best Local Similarity 20.2%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Conservative
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Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                      166 VNHI 169
                                                                                                                                                                                                                                                                                                                                                         118 VNYI 121
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                       RLSRDQAITVLQEEEITAEKSQVSPYGIVAKKGHLASSSLFHD--GVM-----TI 255
                                                                                                                                                                                                              RQGDANVKG-----EEGIVKAHLLIGVHDDIV-SMEYDLAYKLG-DLHPTTHVIS--DIQ 136
                                                                                                                                                                                                                                                                                     137 DFVVALSLEISDEGNITMISFEVROFANVV--NHIGGLSILDPIFGVLSDVLTAIFQDTV 194
                                                                                                                                                                                         31 KAIDDAI----AAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMK 85
                                                                                                                                                        Gaps
                                                                                                                                                        31;
                                                                                                                 7.2%; Score 76.5; DB 4; Length 429; 24.4%; Pred. No. 4.1;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                    84;
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CURRENT APPLICATION DATA:
PAPPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 Best Local Similarity 24.4%; Pred. No. 4.1;
Matches 48; Conservative 34; Mismatches
                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...429
SEQUENCE DESCRIPTION: SEQ ID NO: 3785:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                             195 RKEMTKVLAPAFKRELE 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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                                                                               US-09-107-532A-3785
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                                                                                                               Query Match
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                      120 YKLGDLHPTTHVISDIQDFVVAL--SLEISDEGNITMT-----SFEVROFANV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 KGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH-PTTHVISDIQDFV-VALSLEISDEG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 RGETGVAMAVAQFGEQ----RVEHPRLLRQGTQHVQALHVAGTFPDRVHRGLAVQPRQDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                       8 VMEYKFNLNLKEV-----LPTQGTININGQDNDDDIVIKK---IEFIDSDINVFFYSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GELAMRNIBARGLKOMKROGDANV
                                                              Gaps
                                                                 28;
7.1%; Score 76; DB 4; Length 164; 20.2%; Pred. No. 1.1; ive 30; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 FLDVAG-TAHAFGGFVDHRRG-TLADPVLAHRGD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 NITMISFEVROFANVVNHIGGLSILDPIFGVLSD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 76; DB 24.0%; Pred. No. 8.6; cive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 IDPMKVPD-HADKFERHVGIVDFK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22095, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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ADDRESSEE: GENOME THERAPEI
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) TYPE: PRT
) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22095
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Sequence 5426, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VGIVDFKGELAMRNIEARGLKQM--KRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AGAG---PTASAVVADVIDIVRDISYTEDGAGTIPQLAFBA-----LIMMPILSRE 354
                                                                                                                                                                                                                                                                                                                                                 184 DOHVAAVAVRLVENRRQFLQGVVAVAVİAIAIGGFEHHHVGPAQRRGRAHQRRAGVAEVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGI----ARRAEKGIBLRVHPTLIPDEQLIANVNG----VKNAVLVQANAVGPTLYYGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 YKLGDIHPT-THVISDIQDFVVALSIBISDEGNITMTSFEVRQFANVVNHIGGLSIL--- 175
                                                                                                                                                                                                                                                                                                             5 LLIAAVAFVAVSADPIHYDKITEEINKAIDD-----AIAAIEQSETIDFMKVPDHADKF 58
                                                                                                                                                                                                                                                                                                                                                                                                               ---EARGLKOMKROGDANVK 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AIFODTVRKEMTKVL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 EMTIGYYIRLNAEDQTGVLABVTFILSRAGISIDAIMQQSRLKDLIPIV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 441;
                                                                                                                                                                                                                    Length 423;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                 7.1%; Score 75.5; DE 21.2%; Pred. No. 5.2; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 75.5; DE 23.1%; Pred. No. 5.5; ative 33; Mismatches
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MBER: US 60/094,190
1998-07-27
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US-09-328-352-5426
                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GKHQAARLHLVVELHFD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 GEEGIVKAHLLIGVHDD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.1%
Best Local Similarity 23.1%
Matches 53; Conservative
                                                                                                                                                                                                                                                                  Conservative
  PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331.
SEQ ID NO 21128
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                 ERHVGIVD----
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                        US-09-252-991A-21128
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US-09-134-000C-4810
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US-09-328-352-5426
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/262,991A
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 MRNIBARGLKQMKRQGDANVKGEBGIVKAHLLIGVHDDIVSMEYDLAYKLG--DLHPTTH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 VISDIQDFVVALSLEISDEGNITMTSFEVRQFANV-VNHIGGLSILDPIFGVLSDVLTAI 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 76; DB 4; Length 1196; Best Local Similarity 22.2%; Pred. No. 22; Matches 45; Conservative 41; Mismatches 93; Indels 3
                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: misc_feature
) LOCATION: (B) LOCATION 1...1196
) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:
US-09-107-532A-394
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION WUMBER: 40,489
REFERENCE/DOCKET KUMBER: GTC-012
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 DEMDDEVRTRFKEVFEAIRQEFK 1049
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- FODTVR---KEMTKVLAPAFK 207
                                                                                                                                               COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1196 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3944:
SEQUENCE CHARACTERISTICS:
                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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US-09-252-991A-21128
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       : | |: | : : | : : | 490 NITIGMDNIREQIQDISKRIKRLGESSQEIGDI----VSLINDIADQTNILALNAAIQAS 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SNYDER, DAVID B.

APPLICANT: VAKTARIA, VIKRAM
TITLE OF INVENTION: NOVEL INFECTIOUS BURSAL DISEASE VIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: D. P. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: P.C.
1755 S. Jefferson Davis Highway, Suite 400
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209 TAADDYQFSSQYQS-GGVTI--TLFSANIDAITSL 240
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23.2%; Pred. No. 20;
ve 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kelber, Steven B.
REGISTRATION VINDER: 30,073
REFERENCE/DOCKET NUMBER: 2284-029-0 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/944,943
FILING DATE: 19920915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   154 MTSFEVRQFANVVNHIGGLS 173
                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07944943
Patent No. 5518724
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-944-525-2; Sequence 2, Application US/07944525; Patent No. 563289; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEEX: 248855 OPAT UR
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kelber, Steven B.
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Best Local Similarity
Matches 36; Conserva
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STATE: Virginia
COUNTRY: U.S.A.
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STREET: 17
                                                                                                                                                                                                                                                                                                                 US-07-944-943-2
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                                              임
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREMENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LKQMKRQGDA------NVKGEEGIVKAHLLIGV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 YFATYVFEKGADIPALLGAYILEGSKAGATAASVWAAHHVLPLNVAGYGKLIGAS-IEGS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- ALSLEISD--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | : | | : | HFYNFLNDLTFKVGDKEIEVHTLTHPDFNMVDYVFKEKGNDDLVAMNXLNHDVYDYAS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EGNI-----TMTSFEVRQFANVV------NHIGGLSILDPIFGVLSDV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| ::|| ::|| ::|| ::| | ::| | ::| | :::| | :::| | :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 ADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIG-----VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 QAQ-----EIAGASAAINEMAVSIDQV----SANASESSAVAERSVAIANKGNEVVH 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---T 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 BEINKAIDDAIAAIE--QSETIDPMKVPDHADKFERHVGIVDFK-GELAMRNIBARG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.1%; Score 75.5; DB 4; Length 608;
Best Local Similarity 21.0%; Pred. No. 9;
Matches 56; Conservative 37; Mismatches 71; Indels 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 75.5; DB 4; Length 696; 24.0%; Pred. No. 11; Live 31; Mismatches 74; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 HDDIVSMEYDLAYKLGD----LHPTTHVISDIQDFVV---
; FILE REFERENCE: 032796-032; CURRENT APPLICATION NUMBER: US/09/134,000C; CURRENT FILING DATE: 1998-08-13; PRIOR APPLICATION NUMBER: US 60/055,778; PRIOR FILING DATE: 1997-08-15; NUMBER OF SEQ ID NOS: 6812; SOFTWARE: Patentin version 3.1; SOFTWARE: Patentin version 3.1; LENGTH: 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 LTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 77
US-09-252-991A-16965
; Sequence 16965, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.0%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 DDIVSME---
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                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             rss: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
STREET: 1755 S. JEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino a STRANDEDNESS:
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US-08-219-262B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERARI, STEPHANIE A
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 IEOSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKROGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1012;
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: LUETTICKEN, HEINRICH D.
TITLE OF INVENTION: ATTENDATED, LIVE VACCINE FOR DELAWARE
TITLE OF INVENTION: STRAIN IBDV
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                           COUNTRI.

ZIP: 22202

ZIF: 22202

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/944,525

**TING DATE: 19920914
                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND ADDRESSEE: NEUSTADT, P.C. STREET: 1755 JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR SITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%; Score 75.5; DE 23.2%; Pred. No. 20; tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2284-028-0 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08219262B Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INPORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 20,073
REFERENCE/DOCKET NUMBER: 2284-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-220
TELEFAX: 248855 OPAT UR:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1012 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match '...'
Best Local Similarity 23.2%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-07-944-525-2
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US-08-219-262B-1
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Patent No. 5788970
GENERAL INPORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL.WHERGAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 IEQSETIDEMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKROGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1012;
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SOFTWARE: Petentin Release #1.0, Version #1.30
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR.1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ 1D NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 TAADDYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 TSFEVROFANVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Infectious bursal disease virus
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1012 amino acids
                   (703) 413-2220
                                             TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acid
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                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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; STRAIN: D78
US-08-219-262B-4
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                      TELEFAX:
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Sequence 4, Application US/08219262B
Sequence No. 5788970
GENERAL INFORMATION
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MEMBERG. WIRESHAMIE A
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
THEREON OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-ŢM 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 75.5; DB 1; Length 1012; Best Local Similarity 23.2%; Pred. No. 20; Matches 36; Conservative 35; Mismatches 63; Indels 21
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 2747-047-27
TELECOMMUNICATION: NUMBER: 2747-047-27
TELEPHONE: (703) 413-3000:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 TAADDYQFSSQYQS-GGVTI--TLFSANIDAITSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Infectious bursal disease virus STRAIN: DS326
FILING DATE: 29-PLAN.
CLASSIFICATION: 435
ATTORNEY, AGENT THRORMAINTON:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747.
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
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TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIRGINIA
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-219-262B-2
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US-08-219-262B-4
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Sequence 12. Application US/08219262B
Sequence 12. Application US/08219262B
Sequence 10. 5788970
GENERAL INFORMATION:
APPLICANT: VARHARRA, VIKRAM
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHITERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THERRON CHITERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THERRON THERRON NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEBE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1175. S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 VKAHILIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
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                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                           Length 1012;
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                                                                                                                                                                                                                                              Query Match 7.1%; Score 75.5; DB 1; Length 10 Best Local Similarity, 23.2%; Pred. No. 20; Matches 36; Conservative 35; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F. 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 TAADNYOFSSOY-OTGGVTI--TLFSANIDAITSL 240
STRANS-COOKS: UNKNOW...
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ---NVLVGEGVTVLSLPISYDLGYVRLGDPIPAIGL----DPKMVATCDSSDRPRVYTI 208
157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
                                                                                                                                                                                                                                                                        APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STRET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                       209 TAADNYÕFSSQY-QTGGVTI--TLFSANIDAITSL 240
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209 TAADDYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 75.5; Di
23.2%; Pred. No. 20;
:ive 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PILING DATE: 29-MAR-194
FILING DATE: 29-MAR-194
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEFRX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                      Sequence 1, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: unl
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Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                     US-09-031-655-1
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                                                                                                                                                                                                                                                                          157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08219262B
Patent No. 5788970
GENERAL INFORMATION:
APPLICANT: VAKHERIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MINGEL, WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THERBON
TITLE OF INVENTION: THERBON
TITLE OF INVENTION: THERBON
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                                                                                                                                          40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                  DB 1; Length 1012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/219,262B FILING DATE: US-MAR-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                     209 TAADDYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
                                                                                                                                                                                                                                                                                                                          TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                7.1%; Score 75.5; Dl
23.2%; Pred. No. 20;
ive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 274
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 413-220
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
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Best Local Similarity 23.23
Matches 36; Conservative
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TOPOLOGY: linear
TECHLE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRGINIA
USA
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                                                                      Best Local Similarity
Matches 36; Conserv
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US-08-219-262B-14
    JS-08-219-262B-12
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                                                     Query Match
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US-09-031-655-4
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        Sequence 2, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
APPLICANT: VACHARIA, VIKRAM
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHARRIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHMAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
                                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEPPERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 TAADDYQFSSQYQS-GGVTI--TLFSANIDAITSL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Infectious bursal disease virus
STRAIN: DS326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 75.5; D 23.2%; Pred. No. 20; tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 246855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1012 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.2%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
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US-09-031-655-2
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US-09-031-655-4 Sequence 4, Application US/09031655

RESULT 87

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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
JAPPLICANT: SNYDER, DAVID B
JAPPLICANT: MINDEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMBRIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHARLON CONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAI 189
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APPLICATION NUMBER: US/09/031,655
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F, REGISTRATION NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 41-220
TELECATION OF 850 ID NO: 4:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 4:
LENGTH: 1012 anino acids
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SNYDER, DAVID B
MENGEL-WHERSAT, STEPHANIE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMCDUMTYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         % Sequence 12, Application US/09031655 Sequence 12, Application US/09031655 Patent No. 6017759 Sex Patent INFORMATION: APPLICANT: VAKHAIA, VIKRAM APPLICANT: SNYDER, DAVID B APPLICANT: MENGEL-WHERSAT, STEPHIAPLICANT: MENGEL-WHERSAT, STEPHIAPLIANT: MENGEL-WHERSAT, MENGEL-WHERSAT, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.23
Matches 36; Conservative
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TOPOLOGY: unknow..
MOLECULE TYPE: protein
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Sequence 14, Application US/09031655

Patent No. 6017759

GENERAL INFORMATION:

APPLICANT: VARIARIA, VIKRAM
APPLICANT: SNYDER, DAVID B

APPLICANT: SNYDER, DAVID B

APPLICANT: SNYDER, DAVID B

TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS

TITLE OF INVENTION: THEREON
TITLE OF INVENTION: THEREON

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPITAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEPFERSON DAVID HIGHWAY, FOURTH FLOOR
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
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CHIMBRIC INFECTIOUS BURSAL DISEASE VIRUS CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKRQGDANVKGEEGI
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                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels
                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN FREISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: US/09/031,655 FILING DATE:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 23.2%
Matches 36; Conservative
TITLE OF INVENTION: CHIM
TITLE OF INVENTION: CDNA
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: PatentI
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TOPOLOGY: linear
                                                                                                                                                                            VIRGINIA
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Sequence 24505, Application US/09252991A

Sequence 24505, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT PILING DATE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Indels
                                                                                        COMPUTER READBLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 TAADNYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
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7.1%; Score 75.5; DB
Best Local Similarity 23.2%; Pred. No. 20;
Matches 36; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DAIL:
CLASSPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-MAR-1994
ATTOKNEY/AGENT INFORMATION:
NAME: OBLON NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-2
TELECHONINICATION INFORMATION:
TELEPHONE: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FUNCTH: 1012 amino acids
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; MOLECULE TYPE: protein
US-09-031-655-14
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CRGANISM: Pseudor
US-09-252-991A-24505
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COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US, 69/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US, 60/074, 788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-07-27
                                                                13;
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                                                                                                                                                                                             62 VGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYK 121
                                                                                                                                                                                                                                                                                   122 LGDLHPTTHVISDIQDFVVALSL-EISDEGNITMTSFEVRQFANVVN-HIGGLSILDP-- 177
                                                                                                                                                                                                                                                                                                                          180 AGEL-------AAVDLGALGDLGNLAF--HPGRÓFGNAFQLPTGQLDLADPFP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GVGLLDQQVVLEIEGIEBRHP--VDARABLGDFQLEFLDIAEVVRLFALDPLQFLQRRAQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 DL-AYKLGDLH-PTTHVISDIQDFVVALSLEIS------------DEGNITMTSF 157
                                                                                                                                        146 LGLV----LQLAGSFAEAQGL-----FLAGAE--VAAHLL-----DRGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVERFLLGDLEDEVVHAFAAVAGLAAAAAAAAAGWAGDVLAGGEFLVAGVDDGLPPAAAM
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                                                                                                          6 LIAAV-AFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER---H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 75; DB 4; Length 508; llarity 18.3%; Pred. No. 7.8; Conservative 38; Mismatches 105; Indels
                  7.0%; Score 75; DB 4; Length 482; 28.4%; Pred. No. 7.2; tive 21; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TIDPMKVPDHADKFERHVGIVDFKGELAMRNIE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-17386
; Sequence 17386, Application US/09252991A
; Patent No. 6551795
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; Sequence 6946, Application US/09107532A
; Patent No. 6583275
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SEQ ID NO 17386
LENGTH: 508
                                                              Conservative
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224 QLFGKLADLL 233
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es 54; Conserv
                                         Similarity
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                                                                54;
                  Query Match
Best Local S:
Matches 54,
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Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFRENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NOS: 3340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23213, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF INVENTION:
MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
ADDITION:
GURRENT PERIORS
199-02-18
PRIOR PILING DATE:
1999-02-18
PRIOR PELING DATE:
1999-07-27
NUMBER OF SEQ ID NOS:
33142

SEQ ID NO 23113

LENGTH: 482
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                                                                                                                                                                                                ELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDI-VSMEYDLAYKLGDLHPT 128
                                                                                                                     80 IVLIAGQTPR-----ADLKSKAEQAARTVQKVKNVHNELQVTSPSSLLARNNDAWIT 131
                                                                                                                                                                    ----THVISDIQDFVVALSLEISDEGNIT-----MTSFEVROFANVVNHIGGLSILDPIF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 LRVHPTLIPSQALL------ANVAG----VKNAVMIDAHPLGQSLDYG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAYKLGDLHPTTHVISDIQDFVVALSL------EISDEGNI---TMTS-FEV 159
                         23 SFLSATRDKPIDDDRGTRTIGSKIDDSL--IETKAAVNIAKADPALDK-DSHIVVVSYNG 79
AFVAVSAD-PIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KFLLIAAVAFVAVSADPIHYDKI-TEEINK-AIDDAIAAIEOSETIDPMKVP---DHADK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 458;
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.4<sup>†</sup>
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: M.catarrhalis
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US-09-540-236-3313
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7.0%; Score 75;
19.4%; Pred. No.
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                                                                                                                                                                                   Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 797 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                               ADDRESSEE: Sim & STREET: 6TH Floor CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-433-522A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 96
US-08-433-522A-4
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               APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS PAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 SMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 FERHVGIVDFKGELAMRNIEAR-----GLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 YDAYYDLSQITEEMEVREAAHRYTVFGRVSPQQKKLLVNELKESGRTVAMTGDGVNDVLA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%; Score 75; DB 4; Length 729; Best Local Similarity 20.3%; Pred. No. 14; Matches 40; Conservative 38; Mismatches 89; Indels
                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETID----
                                                                                                                                                                                                                                                                                 COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: ASCII
SOFTWARE: ASCII
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: J4 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: J4 J 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...729
SEQUENCE DESCRIPTION: SEQ ID NO: 6946:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-433-522A-2; Sequence 2, Application US/08433522A; Patent No. 6013514; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 729 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6946:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
GENERAL INFORMATION:
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-532A-6946
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---EGIV-----KAHLLIGVHDDIVSMEY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VRSLFVSGRFDDVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKONLDANGFK-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 SLTFKGNESVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIRDYYLNNGYAKAQI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 VALSLEISDEG---NITMISFEVROF----ANVVNHIGGLSI-LDPIFGVLSDVLTAIFQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKLLIASLLFGTTTTVFAAPFVAKDIRVDGVQGDLEQQIRASLPVRAGQRVTDNDVANI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 EQSETI----DPMKVPDHADKF-----ERHVGIVDFKG-----ELAMRNIEARGLKOM
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APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---IHYDKITEEINKAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                              6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 16;
49; Mismatches
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E: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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                                                                                                                                                                                                    COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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STREET: 61..
TTY: Toronto
                                                                                                                                                                                      STATE: Ontario
                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|
177 SLTFKGNESVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSİRDYYLNNGYAKAQI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.0%; Score 75; DB 3; Length 797; Best Local Similarity 19.4%; Pred. No. 16; Matches 62; Conservative 49; Mismatches 88; Indels 3
 THOMAS, Wayne
YANG, Yan Ping
LOOSMORE, Sheena
SIAA, Dwo Yuan Charles
KUEIN, Michel
VENYION: HAEWOPHILUS OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI---
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: STEWART, Michael I
RECISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECHONENICATION INFORMATION:
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acid
                                                                                                                                    8: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTFRRSDIADVENAIKAKL 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 KRQGDANVKGE-----
APPLICANT: THOMAS, Wayn
APPLICANT: YANG, Yan Pil
APPLICANT: LOCSMORE, Sh
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEI
NUMBER OF SEQUENCES: 55
CORRESSPENDENCE ADDRESSE
ADDRESSEE: SIM & MCBU:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-522A-4
                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                    ADDALL
STREET: 611.
-TV: Toronto
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US-08-433-522A-6
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61 VRSLFVSGRFDDVKAHQEGDVLVVSVVAKSIISDVKIKGNSVIPTEALKQNLDANGFK-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----EGIV-----KAHLLIGVHDDIVSMEY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.0%; Score 75; DB 3; Length 797; Best Local Similarity 19.4%; Pred, No. 16; Matches 62; Conservative 49; Mismatches 88; Indels
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Van Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 12-SEP-1995

CLASSIFICATION: 435

ATTOREX/AGENT INFORMATION:

NAME: STEWARY, Michael I

REGISTRATION NUMBER: 24,973

REFRENCE/FOCKET NUMBER: 24,973

REFRENCE/FOCKET NUMBER: 1038-434 MIS:jb

TELEPRANICATION INFORMATION:

TELEPRANICATION NUMBER: 1038-434 MIS:jb

TELEPRANICATION NUMBER: 1038-434 MIS:jb

TELEPRANICATION OF 6:

SEQUENCE (A16) 595-1163

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE (ARRACTERISTICS:

LENGTH: 797 mains acids
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Patent No. 6083743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-135-166-2
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Sequence 4, Application US/09135166
Patent No. 6083743
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                                                      CHONG, Pele
                                                                                                                                                                             NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCB!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-135-166-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Indels 120; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.0%; Score 75; DB 3; Length 797;
Best Local Similarity 19.4%; Pred. No. 16;
Matches 62; Conservative 49; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI-----
     APPLICANT: THOMAS, Mayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEGURNCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1038-829 MIS: jb
                                                                                                                                                 E: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                      3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INPORMATION:
NAME: STEWART, Michael I
REGISTRATION UNDRER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTVRKEMTKVLAPAFKREL 210
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 KRQGDANVKGE----
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                      Ontario
                                                                                                                                                            STREET: 6TH FA
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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---EGIV-----KAHLLIGVHDDIVSMEY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 120; Gaps
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APPLICANT: CLANCE, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                              STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
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7.0%; Score 75; DB 3;
Best Local Similarity 19.4%; Pred. No. 16;
Matches 62; Conservative 49; Mismatches 81
                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038-829 MIS:jb
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RAIDR APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART Michael I
REGISTRATION NUMBER: 24,973
REFRERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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291 DTFRRSDIADVENAIKAKL 309

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----EGIV-----KAHLLIGVHDDIVSMEY 116
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                                                                                                       APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWARF, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-8
TERECOMMUNICATION INFORMATION:
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TERECOMMUNICATION INFORMATION:
Sequence 6, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: THONG, Pele
APPLICANT: THONAS, Wayne
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 KRQGDANVKGE-----
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TELEFAX: (416) 595-1163
INFORMATION FOR SEG ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / MOLECULE TYPE: protein US-09-135-166-6
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CITY: Toronto
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Db 237 TKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALH----LN 290
Qy 192 DTVRKEMTKVLAPAFKREL 210
Db 291 DTFRRSDIADVENAIKAKL 309
Search completed: August 6, 2004, 16:02:40
Job time: 24 secs
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2 US-10-282-122A-47865
10S-10-282-122A-47865
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Result No.

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ZIP: 02109
COMPUTER READABLE FORM:
 COUNTRY: USA
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US-09-847-208-85
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Publication No. US20020168373A1
GENERAL INFORMATION:
APPLICANT: Wayne R. Thomas and Kaw-Yan Chua
TITLE OF INVENTION: Allergenic Proteins and Peptides From House Dust Mite and Uses Therefor
                                                                                                                                                                                                                                                                                    Sequence 77, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Andrew
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: TGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT FILING DATE: 2001-05-01
NUMBER OF EQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 213
5 US-10-093-463-126
2 US-10-287-122A-68540
2 US-10-282-122A-73215
2 US-10-282-122A-75259
2 US-10-282-122A-76037
2 US-10-282-122A-76037
2 US-10-282-122A-76037
0S-09-815-242-1091
US-10-242-1091
0S-10-369-493-126
5 US-10-369-493-126
4 US-10-219-834-149
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US-09-847-208-77
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                    ALIGNMENTS
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US-10-024-955-7
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100.0%; Score 1068; DB 13; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.8e-102;
Matches 213; Conservative 0; Mismatches 0; Indels 0;
COMPUTER READABLE FORM

MEDIUM TYPE: FICAPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/024,955

FILING DATE: 19-Dec-2001

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/553,336A

FILING DATE: 10-JUN-1996

APPLICATION NUMBER: US/08/553,336A

FILING DATE: 22-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 38,972

TELECOMMONICATION NUMBER: 38,972

TELEDEHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dermatophagoides pteronyssinus (House-dust mite)
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GENERAL INFORMATION:
APPLICANT: Shang, Ke
APPLICANT: Chang, Ke
APPLICANT: Chang, Ke
TILLE OF INVENTION: FUSION MCLECULES AND TREATMENT OF
TILLE OF INVENTION: LGB-MEDIATED ALLERGIC DISEASES;
TILLE REFERENCE: UG67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT PRILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8: SEQ ID NO 105-01
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
TYPE: amino acid
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-12-22
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                                                                                                                                                                                                                                                         30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 NRIAGERISIVEDVEGVTRDRIYTKAEWLNRQFSIIDTGG---IDDVDAPFMEQIKHQAD 77
61 HIGIIDLKGELDMRNIQVRGLKQMKRVGDANVKSEDGVVKAHLLVGVHDDVVSMEYDLAY
                                                                                           61 HVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 103; DB 12; Length 43
23.0%; Pred. No. 0.076;
tive 36; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                        181 VLSDVLTAIFODTVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                      181 VLSDVLTAIFODTVRAEMTKVLAPAFKKELERN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72488, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION

APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.0%
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                              61 HIGIIDLKGELDMRNIQVRGLKQMKRVGDANVKSEDGVVKAHLLVGVHDDVVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMISFEVROFANVNHIGGLSILDPIFG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HVGIVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY 120
                                                                                                                                                                                                              9
                                                                                                                                                                              1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
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Publication No. US20020168373A1
GENERAL INFORMATION:
APPLICANT: WAPTOR R. Thomas and Kaw-Yan Chua
TITLE OF INVENTION: Allergenic Proteins and Peptides From House Dust Mite and Uses Therefor
                          Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.1%; Score 962; DB 13; Length 215;
85.9%; Pred. No. 3.6e-91;
tive 18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
CONPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: BEN PC compatible
OPPERATES SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/024,955
FILING DATE: 19-Dec-2001
CLASSIFICATION: «Unknown»
                                                                                        12; Indels
                      90.1%; Score 962; DB 10;
85.9%; Pred. No. 3.6e-91;
ive 18; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-UNU-1996
APPLICATION NUMBER: US 08/081,540
FILING DATE: 22-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 13H-032CP2
TELEPHONE: (617)742-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLSDVLTAIFQDTVRAEMTKVLAPAFKKELERN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-024-955-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 215 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
                      Query Match
Best Local Similarity 85.9
Matches 183; Conservative
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Best Local Similarity 85.9
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
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APPLICANT: GERLACH, VALERIE L.
APPLICANT: ELLERMAN, KAREN
APPLICANT: BLLERMAN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MATHON OVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOTEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: METHODS OF USING THE SAME FILER REFERENCE: 15966-776CIP
CURRENT APPLICATION NUMBER: US/09/898,570
CURRENT FILING DATE:: 2001-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .62 CKTFILRQLBVAGKEMSEEDVNDMLHÓGKWEVFNESLLTEINÍTKÄQLSEIEQRHKELVN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEG----NITMTSFEVRQFANVVNHI 169
                                                         114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEG----NITMTSFEVRQFANVVNHI 169
                                                                                                162 CKTFILRQLEVAGKEMSEEDVNDMLHQGKWEVFNESLLTEINITKAQLSEIEQRHKELVN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ---LAMRNIEARG-----LKQMKRQGDANVKGEE-----GIVKAHL--LIGVHDDIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 BEINKAIDDAIAAIEQSETID-PMKV-----PDHADKFERHVGIVDF-----KGE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Unknown Organism: POLYX OTHER INFORMATION: hnh0778p17_A1 US-09-898-570-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/198,293
PRIOR PEDING DATE: 2000-04-19
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-06-20
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/204,610
PRIOR PILING DATE: 2000-04-26
PRIOR PELING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
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ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2
SEQ ID NO 30
                                                                                                                                                                                                                                       168 FGLAV 272
                                                                                                                                                                                          170 GGLSI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ELLERWAN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: METHODS OF USING THE SAME
FILE REFERENCE: 1266-776CIP
CURRENT APPLICATION NUMBER: US/09/898,570
CURRENT FILING DATE: 2001-07-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 LGDPYPVSSAHGIGTGDVLDAIVDNLPTEAQEE-----SSDIIKFSLIGRPNVGKSSLI 191
                                                                                      -----ANVV 166
                                             ----SMEYDL-AYK 121
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OTHER INFORMATION: Description of Unknown Organism: POLYX
OTHER INFORMATION: h_nh0778p17_A
US-09-898-570-28
                                                                                                                                                                    122 LGDLHP--TTHVI--SDIQDFVV-ALSLEISDEGNITMISFEVROF
                                                                                                                                                                                                                                                                                                                                              192 NAILGEDRVIASPVAGTTRDAIDTTFTDEEGQEFTMI 228
                                                                                                                                                                                                                                                                                    167 NHIGGLS--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
                                                90 AN-----VKGEEGIVK-----AHLLIGVHDDIV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PRILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR PELING DATE: 2000-04-19
PRIOR PELING DATE: 2000-04-19
PRIOR PELING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/198,645
PRIOR PELING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/199,476
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/204,610
PRIOR APPLICATION NUMBER: 60/209,024
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
PRIOR PELING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/09898570
Patent No. US20020123612A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown Organism
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APPLICANT: GERLACH, VALERIE L.
APPLICANT: ELLERMAN, KAREN
APPLICANT: ELLERMAN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
TYLLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: METHODS OF USING THE SAME FREEKENCE: 15966-776
CURRENT APPLICATION NUMBER: US/09/839,446
CURRENT FILING DATE: 2001-04-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
COTHER INFORMATION: Description of Unknown Organism: POLYX
COTHER INFORMATION: h_nh0778p17_A
US-09-839-446-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: 60/198,293
PRIOR PILING DATE: 2000-04-19

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR PILING DATE: 2000-06-09

PRIOR PILING DATE: 2000-04-26

PRIOR PILING DATE: 2000-04-26

PRIOR PILING DATE: 2000-04-26

PRIOR FILING DATE: 2000-04-26

PRIOR PILING DATE: 2000-04-26

PRIOR PLING DATE: 2000-07-17

PRIOR PLING DATE: 2000-07-17

PRIOR PLING DATE: 2000-07-17

PRIOR PLING DATE: 2001-02-27

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PATCHTIN VET: 2.1

SEQ ID NO 28
                                                                                                                                                                                                                                          Sequence 28, Application US/09839446
Publication No. US20030050232A1
GENERAL INFORMATION:
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 44; Conserva
                 170 GGLSI 174
                                                                                268 FGLAV 272
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FGLAV 272
                                                                                                                                                                                                              US-09-839-446-28
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US-09-839-446-30
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APPLICANT: MACDOUGAAL, JOHN N.
APPLICANT: MACDOUGAAL, JOHN N.
APPLICANT: SMITHSON, GLENNDA
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLECTIDES ENCODING THEM AND
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLECTIDES ENCODING THEM AND
TITLE OF INVENTION: NOVEL HUMAN PROTEINS
CURRENT APPLICATION NUMBER: US/9/998,570
CURRENT PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR PRIOR THING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR PILING DATE: 2001-04-19
----NQIKDLRDLFIQISLLVEEQGESINNIEMTVNSTKEYVNNTKEK 267
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COTHER INFORMATION: Description of Unknown Organism: POLYX
COTHER INFORMATION: CG55655_02
CG-09-898-570-32
                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09898570 Patent No. US20020123612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELLERMAN, KAREN
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ORGANISM: Unknown Organism
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268 FGLAV 272
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222 LB-----
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US-10-012-697-1496
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APPLICANT:
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APPLICANT:
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                                                                                               APPLICANT: GELERALCH, VALEKIE U.
APPLICANT: ELLERALCH, VALEKIE U.
APPLICANT: ELLERALCH, VALEKIE U.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: NEETHODS OF USING THE SAME FILE SERENCE: 15966-776
CURRENT APPLICATION: NUMBER: 60/199, 293
PRIOR APPLICATION NUMBER: 60/199, 45
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/199, 476
PRIOR APPLICATION NUMBER: 60/20, 60/20
PRIOR APPLICATION NUMBER: 60/20, 025
PRIOR APPLICATION NUMBER: 60/20, 025
PRIOR APPLICATION NUMBER: 60/20, 025
PRIOR APPLICATION NUMBER: 60/20, 024
PRIOR FILING DATE: 2000-04-16
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
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PRIOR FILING DATE: 2000-07-17
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9.0%; Score 96; DB 10; Length 294;
Best Local Similarity 23.8%; Pred. No. 0.23;
Matches 44; Conservative 31; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: POLYX; OTHER INFORMATION: hnh0778p17_A1 US-09-839-446-30
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Publication No. US2003005232A1
GENERAL INFORMATION:
APPLICANT: GERLACH, VALERIE L.
APPLICANT: ELLERMAN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GENNDA
Sequence 30, Application US/09839446
                                                                               APPLICANT: GERLACH, VALERIE L. APPLICANT: ELLERMAN, KAREN
                           Publication No. US20030050232A1
GENERAL INFORMATION:
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ORGANISM: Unknown Organism
FEATURE:
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US-09-839-446-32
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: METHODS OF USING THE SAME CURRENCE: 15966-776 (CURRENCE: 159
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9.0%; Score 96; DB 10; Length 294;
Best Local Similarity 23.8%; Pred. No. 0.23;
Matches 44; Conservative 31; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Unknown Organism: POLYX
OTHER INFORMATION: CG55655_02
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Publication No. US20030215803A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
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Scott, Beth
Drmanac, Radoje
Cikvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
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Leshkowitz, Dena
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ORGANISM: Unknown Organism
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BRATCHER, Shawn R. CHEN, Wensheng COHEN, Howard J.
                            Jimmy Y.
DLEY, Diana L
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ORGANISM: Homo sapiens
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## APPLICANT: Kita, David
## APPLICANT: Garcia, Veronica
## APPLICANT: Garcia, Veronica
## APPLICANT: Garcia, Veronica
## APPLICANT: Stache-Crain, Birgit
## TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
## TITLE OF INVENTION: 180LATED FROM HUMAN PROSTATE
## FILE REFERENCE: 2300-16252
## CURRENT APPLICATION NUMBER: US/10/012,697
## CURRENT PILING DATE: 2003-01-21
## PRIOR APPLICATION NUMBER: 60/254,648
## PRIOR APPLICATION NUMBER: 60/254,648
## PRIOR APPLICATION NUMBER: 60/254,648
## RIDK APPLICATION NUMBER: 60/254,648
## RIDK PILING DATE: 2001-03-13
## NUMBER OF SEQ ID NOS: 1568
## SOFTWARE: FastSEQ for Windows Version 4.0
## ILENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.0%; Score 96; DB 15; Length 294 Best Local Similarity 23.8%; Pred. No. 0.23; Matches 44; Conservative 31; Mismatches 58; Indels
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RUSSO, Frank D.
STOCKDREHER, Theresa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEN, Alice
D'SA, Steven A.
AWSHEY, Stefan
DAHL, Christopher R.
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DANIELS, Susan E.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
FONG, Willy T.
GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANZER, SCOCT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purri
CHALUP, Michael S.
CHANG, Simon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IU, TOMMY F.
OSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAFFO, Abel
WRIGHT, Rachel J.
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-697-1496
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268 FGLAV 272
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CONCENT FILING APPLICATION NUMBER: 60/184,777; 60/184,779; 60/184,698; 60/184,770; 60/184,774; 60/184,698; 60/184,770; 60/184,776; 60/184,698; 60/184,776; 60/184,776; 60/184,776; 60/184,771; 60/184,841; 60/184,776; 60/184,771; 60/184,811; 60/184,811; 60/184,772; 60/184,772; 60/186,213; 60/204,863; 60/205,221; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,816; 60/204,816; 60/204,226; 60/205,286; 60/205,286; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,
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OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:204626.1.orf1:2000MAY19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 CKTFILRQLEVAGKEMSEEDVNDMLHQGKWEVFNESLLTEINITKAQLSEIEQRHKELVN 241
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APPLICANT: CCHEN, Howard J.
APPLICANT: HODGSON, David M.
APPLICANT: HINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERANCE: PT-1113 PCT
CURRENT APPLICATION UNMER: US/10/220,120
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9.0%; Score 96; DB 12; Length 314;
Best Local Similarity 23.8%; Pred. No. 0.25;
Matches 44; Conservative 31; Mismatches 58; Indels
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Publication No. US20040142331A1
GENERAL INFORMATION:
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Wright, Rachel J.; Yu, Jimmy Y.;
APPLICANT: Liu, Tommy F.; Yap, Plerre E.;
APPLICANT: Dahl, Christopher R.; Nomiyama, Monika G.;
APPLICANT: Bradley, Dahl, Standey, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
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RESULT 16
US-10-282-122A-54874
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 EEINKAIDDAIAAIEQSETID-PMKV-----PDHADKFERHVGIVDF-----KGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - See File Wrapper or PALM.
APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.; APPLICANT: David, Marie H.; Panzer, Scott R.; APPLICANT: Flores, Vincent Z.; Daffo, Abel; APPLICANT: Marwaha, Rakesh; Chen, Alice J.; APPLICANT: Chang, Sidon C.; Au, Alan P.; APPLICANT: Inman, Rebekah R. TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT FILE REPERENCE: PT-1183 USN CURRENT APPLICATION UNDERF. US/10/363,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

Name / Restaure

OTHER INFORMATION: Incyte ID No: LI:204626.1.orf1:2000SEP08
US-10-363-829-449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.0%; Score 96; DB 16
Best Local Similarity 23.8%; Pred. No. 0.25;
Matches 44; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                  USTRENT HELLLALION NUMBER: US/10/363,829
PRIOR APPLICATION NUMBER: PCT/USO1/2628
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-09-06
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LE-----
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### APPLICATION Identification of Essential Genes in Microcranisms TITLE OF INVENTION: Identification of Essential Genes in Microcranisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PRIOR PTLING DATE: 2000-03-21
PRIOR PRIOR PLICATION NUMBER: 60/206,848
PRIOR PRIOR PRIOR OF E. 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRIOR DATE: 2000-05-26
PRIOR PRIOR FILING DATE: 2000-05-06
PRIOR PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-10-23
PRIOR PRIOR DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/242,576
PRIOR PRIOR DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/242,576
PRIOR PRIOR DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRIOR DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LRFLRLSEVA------EKLOKQAAISIQKGQENYAREMLFQRKKVLQALDKSKRR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MKFLLIAAVAFVAVSADPIHYDKITEBINKAIDDAIAAIEQSBTIDPMKVPDHADKFERH 61
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 241872
LENGTH: 293
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanco, Robert
APPLICANT: Yamanco, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 47; Conserv
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211 QIVELDNPYILLHDKKISSVRDLLTVLDAVAKESKPILIVAEEVBGEALATLVVANIRGI 270
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8.5%; Score 90.5; Di
Best Local Similarity 22.8%; Pred. No. 2.1;
Matches 54; Conservative 43; Mismatches
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                                                                                                                                                                                                         Sequence 17524, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Oblisen, Kari
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , TYPE: PRT
, ORGANISM: Xylella fastidiosa
US-10-369-493-17524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Robert
Forsyth, R.
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Carr, Grant
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Fublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Saleter, Seeven C.
APPLICANT: Slater, Seeven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: BAFRESCION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B1 US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-22
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                            1281 ----FGEDVNKKEFYEENRRTEEDGGKPAQAVPVLLGITKASLGTESFISAASFQDT-- 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVHD--DIVSMEYDLAYKLGDLHPTTHVISDIQDFVVAL-----SLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                               67 FKGELAMRNI-----EARGLKQ-----MKRQGDANVKGE---EGIVKAHLLI--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 FEVROFANVVN------HIGG-----LSILDPIFGVLSDVLTAIFQDTVR 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ---KLGDLHPTTH--VISDIQDFVVALSLEISDEGNITMTSFEVRQFA---NVVNHIGGL 172
                                                                                                                                                                                                                                                                                                       --- MKVPDHADKFERHVGIVD
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                                    Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SEQ TYRARE: PatentIn version 3.1
SEQ ID NO 54874
LENGTH: 1397
                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                            Length 1397;
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                                                                                                                                                                                                                                                                 63; Indels
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8.6%; Score 91.5; DB 12;
Best Local Similarity 21.2%; Pred. No. 6.2;
Matches 53; Conservative 35; Mismatches 63;
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8.5%; Score 90.5; DB
Best Local Similarity 22.8%; Pred. No. 2;
Matches 54; Conservative 43; Mismatches
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Xylella fastidiosa
US-10-369-493-9287
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US-10-369-493-9287
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 2003-02-28
PRIOR PAPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17524
LENGTH: 547
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173 ----SILDPIFG-----VLSDVL-----TAIFQD---TVRKEMTKVLAPPAFKRELEK 212
                                                                                                             271 IKVCAVKAPGFGDRRKAMLEDMAVLTGGTVISEEVGLSLEKATTSHLGKAKKVRVSK 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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979 FNTVLDKVEETVEISGESLENNE----MDKAFFSEIFDNVKGIQENLLTGMFRSIETSIV 1034
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                                                                                                                                                                                                                    1084 -----EQNV-YVDVDVPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESDVITVEEIKD 1135
979 FNTVLDKVEETVEISGESLENNE----MDKAFFSEIFDNVKGIQENLLTGMFRSIEFSIV 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LSLEISDEGNITMTSFEV----ROFANVVNHIGGLS----ILDPIFGVLSDVLTA--IFQ 191
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                                                                           82 KOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVA
                                                                                                               1035 IQSEEKVDLN----ENVVSSIL-----DNIENMKEGLINKLENISSTEGVQETVTEHV--
                                                                                                                                                                                  142 LSLEISDEGNITMTSFEV----ROFANVVNHIGGLS----ILDPIFGVLSDVLTA--IFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Cohen, Joe
APPLICANT: Chen, Joe
TITLE OF INVENTION: Immunogenic Compositions Comprising
TITLE OF INVENTION: Liver Stage Malarial Antigens
TITLE OF INVENTION: Liver Stage Malarial Antigens
TITLE OF INVENTION: Liver Stage Malarial Antigens
TITLE OF INVENTION: Liver Stage Malarial Antigens
TITLE OF INVENTION: Liver Stage Malarial Antigens
CURRENT APPLICATION NUMBER: US/10/415,253
CURRENT FILING DATE: 2003-04-25
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: TANGER OF SEQ ID NOS: 10
SOFTWARE: TANGER OF SEQ ID NOS: 10
SOFTWARE: TANGER OF SEQ ID NOS: 10
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US-09-925-298-445
Sequence 445, Application US/09925298
Sequence 445, Application US/09925298
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
TILE REPERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT APPLICATION NUMBER: DC1/US00/05881
PRICE APPLICATION NUMBER: PCT/US00/05881
PRICE APPLICATION NUMBER: PCT/US00/05881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
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8.4%; Score 90;
Best Local Similarity 23.3%; Pred. No. ...
Matches 47; Conservative 43; Mismatch
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1136 EPVQKEVEKETVSIIE-EMEEN 1156
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1136 EPVQKEVEKETVSIIE-EMEEN 1156
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; Sequence 3, Application US/09742096
; Patent No. US20020155441A1
; GENERAL INFORMATION:
   APPLICANT: DRUILHS, PIERRE
; APPLICANT: DRUILHS, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; CURRENT PELLICANTION NUMBER: US/09/742,096
; PRIOR APPLICANTION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-05-06
; PRIOR FILING DATE: 1998-06-12
; PRIOR FILING DATE: 1998-06-12
; PRIOR FILING DATE: 1998-06-13
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 47806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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27.1%; Pred. No. 4.5;
:ive 19; Mismatches
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                                                                                                                     PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-110-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
                                                  APPLICATION NUMBER: 60/191,078
                                                                              FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
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                         2003-02-20
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US-10-282-122A-47806
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Best Local Similarity 27.1%
Matches 29; Conservative
                                                                        2000-03-2
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; ORGANISM: P. falciparum
US-09-742-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 29
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Best Local Similarity
Matches 47; Conserv
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US-09-742-096-3
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5 셤 ò ď 22 YDKITEBINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGL 81

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APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Dr., Robert C.
APPLICANT: Bast Dr., Robert C.
APPLICANT: Bast Dr., Robert C.
APPLICANT: Bast Dr., Robert C.
APPLICANT: Bast Dr., Robert C.
APPLICANT: Meric, Funda
APPLICANT: Meric, Funda
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APPLICANT: Meric, Funda
CURRENT APLICATION NUMBER: US 60/299,887
FRIOR FILING DATE: 2001-06-21
FRIOR FILING DATE: 2001-06-27
FRIOR FILING DATE: 2001-06-27
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2002-03-05
FRIOR FILING DATE: 2002-03-05
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FRIOR FILING 
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Publication No. US20030096267A1
GENERAL INFORMATION
APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
APPLICANT: Guzman, Luz-Maria
APPLICANT: Guzman, US-MARIA
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFREENCE: 06266-088001
CURRENT APPLICATION NUMBER: US/10/190,279
CURRENT FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US/09/393,858
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8.3%; Score 88.5; DB 14;
Best Local Similarity 24.6%; Pred. No. 2.6;
Matches 30; Conservative 25; Mismatches 50;
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                                                                                                    Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                    Wang, Youznen
Xu, Yongyao
Hoersch, Sebastian
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ORGANISM: Homo sapiens
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GE 194
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US-10-190-279-2
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                                                                                                                                                                                                                                                                                                                                                                 Indels 17;
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                                                                                                                                                                                                                                                                                                     Length 405;
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24.6%; Pred. No. 2.2;
tive 25; Mismatches 50; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 445, Application US/10102806
| Publication No. US20030054421A1
| GENERAL INFORMATION:
| APPLICATION No. US20030054421A1
| APPLICATION NO. US20030054421A1
| TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
| TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
| FILE REFERENCE: PA103PIC1
| CURRENT APPLICATION NUMBER: US/10/102,806
| PRIOR APPLICATION NUMBER: US/925,298
| PRIOR APPLICATION NUMBER: Q09/925,298
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR APPLICATION NUMBER: 60/124,270
| NUMBER OF SEQ ID NOS: 846
| NUMBER OF SEQ ID NOS: 846
| SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                               Query Match

8.3%; Score 88.5; DB 12;
Best Local Similarity 24.6%; Pred. No. 2.2;
Matches 30; Conservative 25; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                   18 DPIHYDKITEEINKAIDDAJAAIEOSETI--
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 846 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 445 LENGTH: 405
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US-10-177-293-140
US-10-177-293-140

Selection No. Mapplication US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
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Matches 30; Conservative
                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-298-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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GE 140
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GE 140
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US-10-102-806-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-102-806-445
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LENGTH: 405
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78 IAMEEADVIVEVVSGKEGITDADEYVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
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138 LGEPLPISSVHGIGTGDVLDAIVENLPNEYEEENPDVIKFSLIGRPNVGKSSLINAILGE 197
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PELLNG DATE: 2000-03-21

PRIOR PELLNG DATE: 2000-03-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

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PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-02-69

PRIOR FILING DATE: 2001-02-69

PRIOR FILING DATE: 2001-02-69

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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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8.2%; Score 88; DB 12;
Best Local Similarity 21.8%; Pred. No. 2.7;
Matches 46; Conservative 34; Mismatches 89
                                                                                            173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
                                                                                                                                                                      198 DRVIASPVAGTTRDAIDTHFTDTDGQEFTMI 228
                                                                                                                                                                                                                                                                                                                                                                                Sequence 74126, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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LENGTH: 436
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8.2%; Score 88; DB 10; Length 436;
Best Local Similarity 21.8%; Pred. No. 2.7;
Matches 46; Conservative 34; Mismatches 89; Indels '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 88; DB 14; Length 39; Best Local Similarity 21.8%; Pred. No. 2.3; Matches 46; Conservative 34; Mismatches 89; Indels
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APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE CF INVENTION: Proteins
TITLE REFRENCE: PWC/P21122WO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: CB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SEQ ID NO 68
LENGTH: 436
             PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 60/099,578
PRIOR FILING DATE: 1996-09-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 68, Application US/09769744A Publication No. US20030134407A1 GENERAL INFORMATION: Le Page, Richard WF APPLICANT: Wells, Jeremy M
                                                                                                                                                                                                                                                                                            TYPE: PRT CORGANISM: Streptococcus pneumoniae US-10-190-279-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
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US-09-769-744A-68
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 DHADKFERHVGI----VDFKGELAMRNI--EARGLKOMKROGDANVKG---EEGIVK---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ------AHLLIGVH-DDIVSMEYDLAYKIGDLH-PTTHVIS----DIQDFV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 AKKYYTLSTBIGGLTFQLSTNKQHMTKEDATQIANEIKHVEGNVDSVEKKVKKSHPKPLY 268
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                                                                                                       PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,525
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2010-10-16
PRIOR PLING DATE: 2010-10-16
PRIOR PLING DATE: 2010-10-16
PRIOR PLING DATE: 2010-10-16
PRIOR PLING DATE: 2010-10-16
PRIOR PLING DATE: 2010-10-16
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8.2%; Score 88; DB 1

Best Local Similarity 19.4%; Pred. No. 5.5;

Matches 60; Conservative 51; Mismatches
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ORGANISM: Staphylococcus haemolyticus
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Publication No. US20030233675A1
GENERAL INFORMATION:
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1 LOCATION: (711)...(711)
2 OTHER INFORMATION: X=any amino acid
US-10-282-122A-71455
                                                                    FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 06286-088001
CURRENT APPLICATION NUMBER: US/10/190,279
CURRENT APPLICATION NUMBER: US/09/393,858
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 43
SOFFWARE: FRSISEQ for Windows Version 4.0
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8.2%; Score 88; DB 14; Length 436;
Best Local Similarity 21.8%; Pred. No. 2.7;
Matches 46; Conservative 34; Mismatches 89; Indels
                                                                                     198 DRVIASPVAGTTRDAIDTHFTDTDGQEFTMI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
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THIE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 71455, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Streptococcus pneumoniae US-10-190-279-5
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10190279
Publication No. US20030096267A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
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122 IGDLHPTTHV----ISDIQDFVVA-LSLEISDEGNITMISFEVRQFANV-----VNHIGG 171
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                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG-
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                                                                                                                                     8.1%; Score 87; DB 12; Length 436;
llarity 22.2%; Pred. No. 3.4;
Conservative 41; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 LS--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
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Publication No. US20040029129A1
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                        ) ORGANISM: Streptococcus pyogenes US-10-282-122A-74394
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Chisen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Famamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                   Similarity
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  LENGTH: 436
TYPE: PRT
                                                                                                                                           Query Match
Best Local S:
Matches 47
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                                                                                                                                                                                                                                                                                                                                                                                                                               26 TEEINKAIDDAIAAIEQSET--ID-PMKVPDHADKFERHVGIVDFKGELAMRNIEARGLK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 OMKRQGDANVKGEEGIVKAHLL--IGVHDDIVSMEYDLAYKLGD----
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                           Query Match

8.2%; Score 87.5; DB 15;
Best Local Similarity 27.8%; Pred. No. 16;
Matches 40; Conservative 19; Mismatches 62;
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1361
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; Sequence 74394, Application US/10282122A
; Publication No. US20040029129A1
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PRIOR FILING DATE: 2006-03-21
PRIOR PELING DATE: 2006-03-21
PRIOR PELING DATE: 2006-03-21
PRIOR PELING DATE: 2006-05-23
PRIOR PELING DATE: 2006-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2006-09-06
PRIOR FILING DATE: 2006-09-09
PRIOR PELING DATE: 2006-09-09
PRIOR PELING DATE: 2006-10-27
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2006-11-27
PRIOR PELING DATE: 2006-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2006-11-27
PRIOR PELING DATE: 2006-11-27
PRIOR PELING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-26
PRIOR PELING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
ARPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3209
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Yamamoto, Robert
Forsyth, R.
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR PILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/257
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PRILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                             Sequence 12179, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT

ORGANISM: Staphylococcus aureus
US-09-815-242-12179
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Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 22.2%
Matches 36; Conservative
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US-10-369-493-7810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 KYPENEIIKTTPNTGERVERGDSVDVVISKGPEKVKMPNVIGLPKEQALQKLKSLGLKDV 469
                                                                                                                                                                                                                                             372 LAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALIRAASKLSSLV- 430
                                                                                                                                                                                                                                                                                                                                   52 PDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDA-----NVKGEEGIVKAHLLI 105
                                                                                                                                                                                       6 LIAAVAFVAVSA-------DPIHYDKITEEINKAIDDAIAAIEQSETIDPMKV 51
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                                                                                Query Match 8.1%; Score 86.5; DB 12; Length 544; Best Local Similarity 24.4%; Pred. No. 5.3; Matches 41; Conservative 21; Mismatches 69; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                                                        106 GVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNIT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVYGDMIEM-----GILDPTKVTRSALQPAASVAGLMITTEAMIT 522
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APPLICANT: Yanamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-27

PRIOR FILING DATE: 2000-12-26

PRIOR FILING DATE: 2000-12-26

PRIOR FILING DATE: 2000-12-26

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PESESEQ for Windows Version 4.0

LENGTH: 660
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llarity 22.2%; Pred. No. 7;
Conservative 31; Mismatches Fo.
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
; ORGANISM: Vibrio cholerae
US-10-282-122A-77547
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Best Local Similarity
Matches 36; Conserv
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Sequence 7810, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 IFSLLMIALVSFVAMAMFGNKYEETPDVIGKSVKEA----EQIFNKNNLKLGKISRSYSD 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ------PDHADKPER--HVGIVDFKG-------ELAMRNIEARGLKQM 84
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| : : | : : | : : | 470 KIEKVYNNQAPKGYIANQSVTANTEIAIHDSNIKLYESLGIK 511
                                                                                                                                                                                                                                                                                                                               APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: AN, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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22.2%; Pred. No. 7.1;
tive 31; Mismatches 50;
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68 KGELAM----RNIEARGLKQMKRQGDANVKGEEGIVKAH-----LLIGVHDDIVSMEYDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845 NGEMILADGRRİVA-----NSANVNGRENVVVIHPDFRMIVLANRPGFPFLGNDFF 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT RILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1018;
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                                                              Sequence 2998, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REPERENCE: HI-A0106
CURRENT APPLICATION NOMER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.0%; Pred. No. 17;
Matches 50; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 55213, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2005-02.
PRIOR FILING DATE: 2000-03-21
PRIOR PEDICATION NUMBER: 60/191, 078
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/20, 335
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 YKLGDLHPTTHVISD---
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Yamamoto, Robert
Forsyth, R.
                                                     JS-10-108-260A-2998
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                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1018
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TILLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 ($5.265.1)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-2-8
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-02-21
SNUMBER OF SEQ ID NOS: 47374
SECURE OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                            274 DAAGERAIRDVVSRGIYAEMRKSNISENGGVYISMAHLGPDDVRRRFKGMVKRCADCGFD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAYKLGDLHPTTH-----VISDIQDFVVALSLEISDEGNITMISFEVRQFANVVNHIG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGDLHPITHVISDIQDFVVALSLEISDEGNIT--MTSFEVROFANVVNHIGGLSILDPIF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LREL---INYLOSISGTFRAAAVELNSVIKATKERESAÉAGEFSELKNAIG-----KÍI 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKITEBINKAIDD-----AIAAIEQSETIDPMKV-PDHADKFERHVGIVDFKGELAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 903;
                                                                                                                                                                                                                                                                                                              8.1%; Score 86; DB 15; Length 527;
llarity 23.5%; Pred. No. 5.7;
Conservative 26; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 66 DFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 85.5; DE 25.0%; Pred. No. 14; tive 30; Mismatches
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7810
LENGTH: 527
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Methanococcus jannaschii
US-10-369-493-1048
                                                                                                                                                                                                                                     ; ORGANISM: Rhodobacter sphaeroides US-10-369-493-7810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.03
Matches 53; Conservative
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Best Local Similarity
Matches 40; Conserv
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CAGUENCE 2. Application US/10423483
Publication No. US2030226154A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Ptacek, Louis
APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Ying-Hui
APPLICANT: Strad841, Shana
ITILE OF INVENTION: MASS 1 GENE, A TARGET FOR ANTICONVULSANT DRUG DEVELOPMENT
FILE REPERENCE: 1321.2.53
CURRENT APPLICATION NUMBER: US/10/220,587
PRIOR FILING DATE: 2003-04-25
PRIOR FILING DATE: 2002-12-02
       453 GTLGDIF-SCHAVDNPKPHSELEMLRQYGPNVPEPILQKLVAAFGELRSLADQGIINY-P 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 KGELAM---RNIEARGLKOMKROGDANVKGEEGIVKAH-----LLIGVHDDIVSMEYDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 NGEMILADGRRIVA-----NSANVNGRENVVVIHPDFRMIVLANRPGFPFLGNDFF 452
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                                                                              ---IQDFVVALS--LEISDEGNITMTS 156
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Edin D.
APPLICANT: Tahy, Edin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gleen, Gary W.
APPLICANT: Gleen, Gary W.
APPLICANT: Gleen, Gary W.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILE REFERENCE: 660081465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: 103-04-04
NUMBER OF SDD NOS: 3077
SOFTWARE PASISED FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 1441;
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22.0%; Pred. No. 27
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                                                                              120 YKLGDLHPTTHVISD-----
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ORGANISM: Homo sapiens
US-10-408-765A-824
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Matches 50; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                    See File Wrapper or PALM
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                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Indels
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,9
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See NUMBER OF EXC ID NOS: 78614
SOFTWARE: Patentin version 3:1
SEQ ID NO 55213
LENGTH: 1396
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1 Similarity 23.6%; Pred. No. 26;
49; Conservative 34; Mismatches
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Best Local Similarity 22.0%; Pred. No. 27;
Matches 50; Conservative 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION

PUBLICATION NO. US20040038325A1

GENERAL INFORMATION:

APPLICANT: PHELPS, CHRISTOPHER BENJAMIN

APPLICANT: GUTTERLOSE, ALEX

APPLICANT: GUTTERLOSE, ALEX

TILLE OF INVENTION: ADHESION MOLECULES

FILE REFERENCE: 674575-2001

CURRENT APPLICATION NUMBER: US/10/346,863

CURRENT APPLICATION NUMBER: PCT/GB01/03318

PRIOR APPLICATION NUMBER: PCT/GB01/03318

PRIOR APPLICATION NUMBER: GB 0018126.3

PRIOR APPLICATION NUMBER: GB 0018126.3

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-10-17
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                                                                                                                                                                                                                                                                                                                                        ), ORGANISM: Chlamydia trachomatis
US-10-282-122A-55213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-346-863-6
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 49; Conserv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-346-863-6
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; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7986
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                                               : : : : : 2677 NVTYATVPGIVS 2688
                       176 DPIFGVLSDVLT 187
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Best Local Similarity
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                             US-10-369-493-18437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-369-493-18437
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US-10-369-493-7986
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APPLICANT: White, H. Steve
APPLICANT: White, H. Steve
APPLICANT: White, H. Steve
APPLICANT: Stradski, Shan
APPLICANT: Stradski, Shan
TITLE OF INVENTION: MASS 1 GENE, A TARGET FOR ANTICONVULSANT DRUG DEVELOPMENT
TITLE OF INVENTION NUMBER: US/10/220,587
CURRENT APPLICATION NUMBER: US 60/187,209
PRIOR APPLICATION NUMBER: US 60/187,209
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID MOS: 33
SOFTWARE: PATENTIN Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2508 TVTVNILLANDNVAGIVSFQTASRSVIGHEGEMLQFHVVRTPPGRGNVTVNWKVVGQNLEV 2567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2617 PAGVALLDAQGYAAVLTVEASDEPHGVINFALSSRFVVIQEANVTIQLFVNREFGSIGAI 2676
                                                                                                                                                                                                                                                                                                                                                                                                                  79 RGLKQMKRQGDANVKGE----EGIVKAHLLIGVHDDIVSME-----YDLAYKLGDLH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 PTTHVISDIQDFVVALSLEISDEG----NITMTS-FEVRQFANVV-----NHIGGLSIL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGLKQMKRQGDANVKGE----EGIVKAHLLIGVHDDIVSME-----YDLAYKLGDLH 126
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                                                                                                                                                                                                                                                                                                                                  26 TEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHV-----GIVDFKGELAMRNIEA 78
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                                                                                                                                                                                                                                                                                          41; Gaps
                                                                                                                                                                                                                                                 Length 2780;
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                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                 DB 12;
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.4%; Pred. No. 70;
Matches 41; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
PRIOR APPLICATION NUMBER: US 60/187,209 PRIOR PLING DATE: 2000-03-03 PRIOR APPLICATION NUMBER: US 60/222,898 PRIOR FILING DATE: 2000-07-03 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10220587
Publication No. US20030208782A1
GENERAL INFORMATION:
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                                                                                                                                           ; LENGTH: 2780
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-423-483-2
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US-10-220-587-2
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Best Local Similarity
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SEQ ID NO 2
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Matches
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfenng
APPLICANT: Chen, Xianfenng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: WINBER: US 10(5.05.2) B
CURRENT PELLING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO : 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 ALROMSAPSAKVLR-----ANGEKTSIPARBLVVG---DIVSLE-----AGDFIPADG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 VISDIQDFVVALSLEISDEGNITMTSFEVROFANVV------NHIGGLSILDPIFG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 VLSDVLTAIFQDTVRKEMTKVLAPA-----FKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 RADFLVTÁTAEQTEIGKIAQMLETÁEAKQTPLQQKLEK 238
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21.7%; Pred. No. 5.1;
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Best Local Similarity 24.7%; Pred. No. 15;
Matches 39; Conservative 33; Mismatches 44
Sequence 18437, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7986, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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APPLICANT: Zhou Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILHKRVIGQNDAVNSISKAVRRARAGLK----DP-----KRPIGSFIFLGPTG 548
18 DPIH-----YDKITEEINKALDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                           73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY
                                                                                                                                                                                                                                                                           16 SADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGI-VDFKGELAMR
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7.8%; Score 83.5; DB 12; Length 281;
Best Local Similarity 22.8%; Pred. No. 4.2;
Matches 51; Conservative 36; Mismatches 74; Indels 63
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US-10-424-599-160426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
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| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Soumitra S.
| APPLICANT: Eaby, Eoin D.
| APPLICANT: Zhang, Bing |
| APPLICANT: Zhang, Bing |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Glenn, Gary M. |
| APPLICANT: Glenn, Gary M. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 160426, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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US-10-408-765A-1398
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APPLICANT: Forsyth, R.
APPLICANT: Au, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REPRENCE: ELITTA.034A
CURRENT APPLICATION NUMBER: US/10/202,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : :|: : | ; : :| : :| : :| : :| | | ; : :| | | ; : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : 
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                                                                                                                                                                                                8 AAVAFVAVSADPIHYDKITEEINKAIDDALAAIEQSETIDPMKVPDHADKFERHVGIVDF 67
                                67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
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                                77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 GLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFK 207
                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71072, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-71072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Faming
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Best Local Similarity 23.0%
Matches 50, Conservative
                                     47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
US-10-282-122A-71072
                                          Matches
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--NVVNHIGGLSILDPIFGVLSDVLTAIFQDTV 194
                                               294 IGRI-INSDBVQSVVKPLNKEVKREKRKNPLKNVAAVLKLNPYFG-----TA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 YAEAFE----IQPFSGEDSFVTLKGSDFKDALEQ-----QWEEGSARPVAALGVSDN-VS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 MEYDLAYKLGDLHPTTHVISDI-----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.8%; Score 83.5; DB 9; Length 412; Best Local Similarity 31.5%; Pred. No. 7.3; Matches 34; Conservative 16; Mismatches 41; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PLILNG DATE: 1999-12-16
PRIOR PLILNG DATE: 2000-4-07
PRIOR PLILNG DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
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Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                Sequence 3526, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Corynebacterium glutamicum
                                                                                                                                                            341 RKMATLAEAARIKARKEK 358
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                            195 RKEMTKVLAPAFKRELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                  HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
             149 EGNITMISFEVROFA-
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Wall, Daniel
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SOFTWARE: Patentin ver. 3.(
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Carr, Grant
Yamamoto, Rober
Forsyth, R.
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US-09-738-626-3526
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SRLTAMKMODEMRIMEEELRDYQRAQDEALTKROLL---EQTLKDLEYELEAKSHLKDDR 117
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237 VE---RINLIDLAPGGHLGRFVIWTESAFKKLJEEVYGTFEAPSLKKKGFILPRPKMANAD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HLGKTIEKLQKEMADIVBASRTSTLELQNQLDEYKEKNRRE--LAEMQRQLKEKTLBAEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                21 HYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKPERHVGIVDFKGELAMRNIEAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IAAVAFVAVSADPI-----HYDKITEEINKAIDDALAAIEQ-SETIDPMK-VPDHAD--
                                                                                                                                                                                                                                                                                                                                7.8%; Score 83.5; DB 16; Length 360;
21.7%; Pred. No. 6;
ive 29; Mismatches 66; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 83.5; DB 16; Length 405; 24.8%; Pred. No. 7.1; tive 35; Mismatches 82; Indels 77
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660089.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1398
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT4530_66589C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6; ; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 -GLKOMKROGDANVKGE.
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                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-408-765A-1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Thes 64; Conservat
                                                                                                                                                                                                                                                                                                                                                     Similarity
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Best Local Simi
Matches 31;
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| Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 13423 | Sequence 134622 | Sequence 134622 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 13423 | Sequence 134622 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 134623 | Sequence 1346363 | Sequence 1346363 | Sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 GGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAF--KRELEK 212
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US-10-437-963-134622
                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_12903C.1.pep
US-10-437-963-108671
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ORGANISM: Oryza sativa
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Sequence 108671, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bring Barbazuk, Brad
APPLICANT: Bring Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Rice Nucleic Acid Molecules
TITLE OF INVENTION: Rice Nucleic Acid Molecules
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SOFTWARE: Patentin version 3.1
SEQ ID NO 78505
LENGTH: 548
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                                 FILE REFERENCE: ELLIFACONTONERS: US/10/282,122A CURRENT PEDLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR PELING DATE: 2003-02-20 PRIOR PILING DATE: 2000-05-23 PRIOR PELING DATE: 2000-05-23 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-05-26 PRIOR PELING DATE: 2000-09-06 PRIOR PELING DATE: 2000-09-06 PRIOR PELING DATE: 2000-09-06 PRIOR PELING DATE: 2000-09-09 PRIOR PELING DATE: 2000-09-09 PRIOR PELING DATE: 2000-10-23 PRIOR PELICATION NUMBER: 60/242,578 PRIOR PELING DATE: 2000-110-23 PRIOR PELICATION NUMBER: 60/253,625 PRIOR PELING DATE: 2000-112-22 PRIOR PELING DATE: 2000-112-22 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR PELING DATE: 2001-02-09 PRIOR PELING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR PILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 PRIOR PRIOR FILING DATE: 2001-02-09 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR
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US-10-366-493-14213
US-10-366-493-14213
US-10-366-493-14213
US-10-369-14213, Application US/10369493

Publication No. US20030233675A1

SEQUENCE 14213, Application US/10369493

Publication No. US200323675A1

APPLICANT: Cao, Yongwei

APPLICANT: Stater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(5205.)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14213

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    550 DKVSETDRKAIEDAIASLKTAVEAAE------PDADDIQAKTQTLMEVSMKLGQAIYEA 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 633;
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                   - | | : | : | : - DDVVDADYE 624
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Best Local Similarity 28.3%; Pred. No. 15;
Matches 28; Conservative 16; Mismatches 27;
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TYPE: PRT
7 ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14213
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         | | | : | : | 603 ----QQAEAGDASAEGK-
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US-10-369-493-14987
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Sequence 11797, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yorgwei

APPLICANT: Cao, Yorgwei

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: 1940/35052) BI

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374
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Sequence 14521, 242

Publication No. US20030233675A1

Publication No. US20030233675A1

GENERAL INRORMATION:

APPLICANT: Cao, Vongwei

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Steven C.

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---GKPDPFLFQIKDKLAALYLEGCKAEKGEPLPVGLVDMRELKK 474
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; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11797
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US-10-369-493-11797
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MSJUL 389-566-1559

WS-10-389-566-1559

WS-10-389-566-1559

Sequence 1559, Application US/10389566

Publication No. USZO040025202A1

GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC

APPLICANT: Laurie, Cathy C

TTLE REPERENCE: 38-77/52900)

CURRENT APPLICATION NUMBER: 2003-03-31

PRIOR FILING DATE: 2002-03-35

PRIOR PLING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR PLING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOUTHWARE PARENCE: 3002-06-26

NUMBER OF SEQ ID NOS: 2459

SEQ ID NO 1559

LENGTH: 633
550 DKVSETDRKAIBDAIASLKTAVEAAB-----PDADDIQAKTQTLMEVSMKLGQAIYEA 602
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LEISHMANIA LACOR
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 845
                                                                       79 RGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
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                                                                                                                                           ----- DDVVDADYE 624
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; ORGANISM: Agrobacterium tumefaciens
US-10-389-566-1559
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Patent No. US20020081320A1
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Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
Probst, Peter
                                                                                                                                       603 ----QQAEAĞDASAEĞK---
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ORGANISM: Leishmania major
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LOCATION: (1)...(845)
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APPLICANT:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
SRIOR FILING DATE: 2003-02-21
SRIOR FILING SAIR: APPLICATION NUMBER: US 60/360,039
PRIOR FILING SAIR: 2002-02-11
SEQ ID NOS: 47374
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| Publication No. US20040025202A1
| GENERAL INFORMATION:
| APPLICANT: Monsanto Technology, LLC
| APPLICANT: Laurie, Cathy C
| TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
| FILE REFERENCE: 38-77 (52900) D
| CURRENT APPLICATION NUMBER: US/10/389,566
| CURRENT APPLICATION NUMBER: US 60/365,301
| PRIOR APPLICATION NUMBER: US 60/365,301
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-26
| NUMBER OF SEQ ID NOS: 2459
| SEQ ID NO 1416
| LENGTH: CATHOL OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF CATHOLOGY OF 
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7.8%; Score 83; DB 16; Length 633;
Best Local Similarity 28.3%; Pred. No. 15;
Matches 28; Conservative 16; Mismatches 27; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 83; DB 15; Length 633; 28.3%; Pred. No. 15; Live 16; Mismatches 27; Indels ;
                                                                   603 ----QQAEAGDASAEGK-------DDVVDADYE 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 RGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
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79 RGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
                                                                                                                                                                                                                                             Sequence 15263, Application US/10369493
Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Agrobacterium tumefaciens US-10-369-493-15263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 28.33
Matches 28, Conservative
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-10-389-566-1416
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                                                                                                                                                                                                                                     89 DANV----KGEEGIVKAHILIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSI 144
                                                                                                                                                                                                                                                                            53 DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
                                                                                                                                                                                                                                                                                                                          145 BISDEGNITMTSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP 204
                                                                                                                                                                                                                                                                                                                                                        101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP 151
                                                                                                                                                                                    2 VNFTVDQVRELMDYPDQIRNMSVIAHVD-----HGKSTLSDSLVGAAGIIKWEEAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 EISDEGNITMTSFEVRQFANVANHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
                                                                                                                   34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Blatia, Ajay
APPLICANT: Datia, Ajay
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
TILLE OF INVENTION: LEISHWANIA ANTICENS FOR USE IN THE
TILLE OF INVENTION: LEISHWANIA ANTICENS FOR USE IN THE
TITLE OF INVENTION: LEISHAAN AND DIAGNOSIS OF LEISHWANIASIS
FILE REFERENCE: 210121.420C9
CURRENT APPLICATION NUMBER: US/09/991,496
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 137
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS 103
LENGTH: 845
                                                              7.8%; Score 83; DB 9; Length 845; 23.3%; Pred. No. 23; cive 34; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.8%; Score 83; DB 9; Length 845; Best Local Similarity 23.3%; Pred. No. 23; Matches 42; Conservative 34; Mismatches 70; Indels
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT; LOCATION: 315, 324; OTHER INFORMATION: Xaa = Any Amino Acid US-09-991-496-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110, Application US/09991496
Patent No. US20020169285A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
                                              Query Match
Best Local Similarity 23.3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
  ; OTHER AME ON US-09-874-923-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-991-496-110
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APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Pind APPLICANT: Li, Pind TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE PETERENT APPLICATION NUMBER: US/10/437,963 CURRENT PILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 ELENGTH: 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18650, Application US/10369493
Sequence 18650, Application US/10369493
Publication No. US2003023367541
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GEO, YORGWEI
APPLICANT: GIAter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: GOLdman, Barry S.
APPLICANT: GOLDMAN: BARRSSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 1003-02-28
PRIOR PEDICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ. ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |: || :: | | :: || 346 LRALLEVTINDWPA-LSNLSQSNKGYKAYTHCMDETETNNPVRKKGKHFEHTADHRTKP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 KHRSGKTVF-----ATVKGLKVVFGKGPGSQPIECEDGVYGKSKHTLEARNDLKHIE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 YDLAYXLGDLHPT----THVIS------DIQDFVVALSLEISDEGNI-TMTSF 157
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7.7%; Score 82.5; DB 15; Length
Best Local Similarity 19.9%; Pred. No. 53;
Matches 40; Conservative 37; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_10506C.1.pep
US-10-437-963-106024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
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7.7%; Score 82.5; DE
Best Local Similarity 19.6%; Pred. No. 26;
Matches 44; Conservative 48; Mismatches
La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Çao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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US-10-369-493-13650
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Sequence 106024, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:

RESULT 62 US-10-437-963-106024

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APPLICANT: Gerrach, valette
APPLICANT: Gerrach, valette
APPLICANT: Gerrach, David W.
APPLICANT: Gateron, David W.
APPLICANT: Cateron, David W.
APPLICANT: Cateron, Elina
APPLICANT: Cateron, Elina
APPLICANT: Cateron, Elina
APPLICANT: Lepte, Mario W.
APPLICANT: Allobrook, Uodan P.
APPLICANT: Allobrook, Uodan P.
APPLICANT: Allobrook, Uodan P.
APPLICANT: Burgess, Catherine M.
APPLICANT: Burgess, Catherine M.
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APPLICANT: Burgess, Catherine M.
APPLICANT: Burgess, Catherine M.
APPLICANT: Burgess, Catherine M.
APPLICANT: 2001-03-07
CURRENT APPLICANTON WHERE: USSN 60/243,322
PRIOR APPLICANTON WHERE: USSN 60/238,675
PRIOR APPLICANTON WHERE: USSN 60/238,675
PRIOR PLING DATE: 2001-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 894, Application US/10289762; Publication No. US20040006218A1; GENERAL INFORMATION:
Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
Guo, Xiaojia Sasha
Tchernev, Velizar T.
Fernandes, Elma R.
                                                                                                                                                                                                                                  Casman, Stacie J.
Malyankar, Uriel M.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-092-900A-218
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US-10-289-762-894
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Best Local S
Matches 39
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; Sequence 244, Application US/10116275
; Publication No. US20030211476A1
; Deblication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Blam Pharmaceutical Technology
; APPLICANT: Brayden, David
; APPLICANT: Lambkin, Imedda
; APPLICANT: Lambkin, Imedda
; APPLICANT: Lambkin, Imedda
; APPLICANT: Lambkin, Imedda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: Blo67/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT APPLICATION NUMBER: US/10/116,275
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
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                                                                                                                                                                                                                                                                                                 || | :::|:
|-----HIEGGDVVEPLGERVLGR 842
    686 WSKANDEVSKAM---MANLSKEKVID-----RHGDEVEQE----SFNSMYMMADSGARGS 733
                                                                                                                                          ::|: | | | | : | : | : | : | : | | | : | : | : | | | | : | : | | | : | : | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                          126 HPTTHVISDIQDFVVALSLBISDEGNITMISFEVRQFANVVNHIGGLSILDPI-FGVLSD 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 S-----LEISDEGNITMTSFEVRQFANVVNHIGGLSIL 175
                                                                                        81 ---LKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEY---
                                                                                                                                                                                                                                                                                                     794 GYLTRRLVDVAQDLVVTEIDCGTEHGLLMTP---
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Speck, Sureeh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li, Li,
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Greev, Vladimir Y.
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                          185 VLTAIFQDIVRKEMTKVLAPA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              843 V---IARDVFKPGTEDVIVPA 860
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Miller, Charles E.
Kekuda, Ramesh
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ORGANISM: Homo sapiens
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US-10-092-900A-218
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APPLICANT: XU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-21
PRIOR PILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/291,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
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PRIOR PELING DATE: 2001-02-16
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|333 MDYSAIPSVIFTHP-----BIAMVGLSLQBAEQQNLPAKLIKFPFKAIGKAVALGAS 384
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              385 DGFAAIVSHEITQQILGAYVIGPHASSLIGEWTL----AIRNELT 425
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                                                                                                                                                                     Sequence 54983, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amalone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Cheryl
APPLICANT: Cheryl
APPLICANT: Cheryl
APPLICANT: Grade, Wali
APPLICANT: Grade, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grade
APPLICANT: Yanamoto, Robert
APPLICANT: Porsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54983
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APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ-----
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Sequence 399, Application US/09841132
Patent No. US2020061848A1
Sequence 399, Application:
Sequence 399, Application:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT FILLING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: PastSEQ for Windows Version 3.0/4.0
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                                                                                                                                                                                                                                                                                                                                                                               7.7%; Score 82; DB 15; Length 397; 20.4%; Pred. No. 9.9; ive 44; Mismatches 69; Indels
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// Pred. No. 12;
44; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 --FANVVNH----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 82; 20.4%; Pred. No.
                                                                                                                                                                                                                                                                  TYPE: PRT

/ ORGANISM: Chlamydia pneumoniae

US-10-289-762-894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Chlamydia pneumoniae US-09-841-132-399
                                                                                                                                                                                                                                                                                                                                                         46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-841-132-399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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57 KFERHVGIVDFKGELAMRNIEARGLKQMKRQGDANV------KGEEGIVKAHLLIGV 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 TRDSIYVDFERGGKPYTLIDTAGLRRRGKVFEAIEKFSVVKTLQSISDANVVILLLDARQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:|:|:|:|:|
-----ARGVK-IAIVGRPNVGKSTLINALVGEERVI-AFDMPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MKFLLIAAVAFVAVSADP----IHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10046649
| Publication No. US20030073094A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Stress Proteins and Uses Therefor NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
| STREET: A Militia Drive CITY: Lexington STREET: USA COUNTRY: USA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6%; Score 81.5; DB 12; Length 4 Best Local Similarity 24.2%; Pred. No. 13; Matches 47; Conservative 26; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Burkholderia fungorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 -FANVVNHIGGLSI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 DISEQDAHIAGEVV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 ITMTSF-----VNHIGGLSIL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GIVDFK-GELAMRN---IEARGL--KOMKROGDANVKGEEGIVKAHL--LIGVHDDI--V 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 NTLDIEYGDQMVTSDYMIQLRDLLYKVMTQGGNANLTALSIFMESHIEAFISVLDQIKQT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 SME-----YDLAYKLGDLH--PTTHVISDIQD----FVVAL-----SLEISDEGN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 QTLYBFRSANPKALNSLEASGVFGTYRLTTNYRSNQEILDFANIHLSDIEANQFAGIQLY 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IAAVAFVAVSADPI--HYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDH-ADKFERHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 82; DB 9; Length 785; 23.6%; Pred. No. 26; tive 38; Mismatches 80; Indels
                                                                                APPLICANT: NAKAGARA, SATOSHI
APPLICANT: NAKAGARA, SATOSHI
APPLICANT: ANDO, SERXO
APPLICANT: ANDO, SERXO
APPLICANT: ANDO, SERXO
APPLICANT: CCHIAI, KEIKO
APPLICANT: CCHIAI, KEIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NAKO
APPLICANT: TATEISHI, NASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PELING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 ANSF----DAPTADSFKEKVELDMHHV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 DPIFGVLSDVLTA-IFQDTVRKEMTKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49547, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 23.61
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-738-626-5445
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Gaps

17;

Length 745; Indels

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77 EARGLKQMKRQGDANVKGEEGIVKAHLL----IGVHDDIVSMEYDLAYKLGDLHPTTHVI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 SDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIG---GLSILDPIFGVLSDVLTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 52455
                                                                                                                                                                                                                                                                                                                                                     DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                 Query Match 7.6%; Score 81.5; Di
Best Local Similarity 25.2%; Pred. No. 27;
Matches 30; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 81.5;
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2657
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-282-122A-52455

; Sequence 52455, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/201, PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-52455
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFIBINS IN PLANTS FOR PRODUCTION OF
FILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EGNITMTSFEVRQ 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 PETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 FANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VVNTIRGIVKVAAVKAPGFG---DRRKAMLODIATLTGGTVISBEIGMELEK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 547;
                                                        MEDIUM ITER: FIOPY GISK

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/046,649

FILING DATE: 14-Jan-2002

CLASSIFICATION A35

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/336,251

FILING DATE: 04-JUN-1993

APPLICATION NUMBER: US 07/804,632

FILING DATE: 09-DEC-1991

APPLICATION NUMBER: US 07/26,581

FILING DATE: 15-JUN-1989

APPLICATION NUMBER: US 07/206,581

FILING DATE: 15-JUN-1989

APPLICATION NUMBER: US 07/206,581

FILING DATE: 15-JUN-1989

APPLICATION NUMBER: US 07/206,581

FILING DATE: 15-JUN-1989

ATTORNEY/AGENT INFORMATION:

NAME: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISCRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.6%; Score 81.5; Di
20.4%; Pred. No. 18;
tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 547 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-046-649-2
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Length 1279;

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117 --DLAYKIGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIG---- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VKAHLL--IGVHDDIVSMEYDL--------AYKLGDLHPTTHVISDI 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ODFVVALSLEISDEGNITMISF-----EVROFANVVNHIGGLSILDPIFGVLS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 EQSETIDPMKVPDHADKF--ERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trindur, Donald E.
APPLICANT: Trindur, Donald E.
APPLICANT: Whited, Gregory M.
APPLICANT: Selifonova, Olga V.
TITLE OF INVENTION: Mutant 1,3-Propanediol Dehydrogenase
FILE REFERENCE: GC580-2D1
CURRENT APPLICATION NUMBER: US/09/991,138
CURRENT APPLICATION NUMBER: US 09/570,778
PRIOR PLILING DATE: 2000-05-14
PRIOR PLILING DATE: 1999-05-19
PRIOR PLILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Indels
                                                                                                                                                                                                  FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(296)

OTHER INFORMATION: unsure at all Kaa locations
FEATURE:

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_58074C.1.pep
US-10-424-599-239257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 81; DB 12;
; Pred. No. 8.3;
37; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ---- DVLTAIFQDTVRKEMTKVL 202
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; ORGANISM: Clostridium pasteurianum
US-09-991-138-12
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 21.6%;
Matches 44; Conservative 3
                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                             NUMBER OF SEQ ID
SEQ ID NO 239257
LENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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Sequence 197313, Application US/2040031072A1
Sequence 197313, Application No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ex Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2033-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 197313
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                                                                                                                                           75 ----NIEARGLKOMKROGDANVKGEEGIVKAHLLIGV-----HDDIVSMEYDLAYKL 122
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                                                                                                      23 DKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMR----
                                        Gaps
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------VNDIE------BIXNRYEI-----QIXYYEEALNRITGKNVKD 1264
                                                                                                                                                                                                                                                                                                                                                                                 123 GDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILD 176
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                                        61;
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                                        47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_201C.1.pep
US-10-424-599-197313
; Pred. No. 60;
26; Mismatches
Best Local Similarity 23.0%;
Matches 40; Conservative 2
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-197313
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73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTH-- 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2000-12-29
PRIOR PELING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:::||: ;
212 ECEMEKPYILIYDKKISNLKDFLPILEPAVQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 IAEDVDSEALTTLVVNRLRSQLKICAVKAPGF 281
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LANT: YUE, Henry
Mariah R.

APPLICANT: LAL, Preet;
APPLICANT: LAL, Preet;
APPLICANT: DATERSON, Chandra
APPLICANT: BATTERSON, Chandra
APPLICANT: BATTERSON, Chandra
APPLICANT: BANDMAN, Olga
APPLICANT: MATHUR, Preete
APPLICANT: MATHUR, Preete
APPLICANT: RADDY, Roopa
APPLICANT: REDDY, Roopa
TITLE OF INVENTION TRANSCRIPTION FACTORS
FILE REPERENCE: PF-O751 PCT
CURRENT FILING DATE: 2001-03-13
NUMBER: OF SEQ ID NOS: 214
SOQ ID NO 23
LENGTH: 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
7.6%; Score 81; DB 1
Best Local Similarity 20.3%; Pred. No. 20;
Matches 43; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 PIFGVLSDVLTAIFQDTVRKEM--TKVLAPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/10221625 Publication No. US20040033942A1 GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT / ORGANISM: Bacteroides fragilis US-10-282-122A-48944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 48944
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APPLICANT: Cac, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10081
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: magnetite-containing magnetic coccus US-10-369-493-10081
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Publication No. US20040029128A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                      ; Seguence 10081, Application US/10369493 ; Publication No. US20030233675A1
                                                    171 GLSI-----LDPIFGVLSDV 185
                                                                                                         315 GLSVMEAAEKAIDAMFRLSKDV 336
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
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Gaps

54;

82; Indels

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Query Match
Best Local S:
Matches 41
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TITLE OF INVESTION: Identification of Essential Genes in Microorganisms
TILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                          Ouery Match 7.6%; Score 81; DB 12; Length 767; Best Local Similarity 22.9%; Pred. No. 32; Matches 36; Conservative 29; Mismatches 56; Indels
                                                              | NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20040033942A1 1359294CD1
| US-10-221-625-23
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ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamddio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Carr, Grant
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                                                                          64 IVDFKGEL---AMRNIEARGLKOMKRQGDAN------VKGEEGIVKAHLLI---GVH 108
                                                                                                                                                                                         109 DDIVSMEYDLA-YK-----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                        72 AMRNIEARGLK---OMKROGDANVKGEEGIVKAHLLIG---VHDDIVSMEYDLAYKLGDL
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14 RKFDDAVSNGVAAPADVDLSLLEAIEKSQNAVEALDLRALKKHVLSFERRL---
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Length 245;
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24.6%; Pred. No. 11;
Live 32; Mismatches 60; Indels
                                                69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Clone ID: PAT_MRT3847_202C.1.pep
US-10-424-599-197424
; Score 80.5; DE
; Pred. No. 7.1;
35; Mismatches
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APPLICANT: Kovalic, David K.; APPLICANT: Zhou, Yihua; APPLICANT: Cao, Yongwei; APPLICANT: Boukharov, Andrey A.; APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-197424
US-10-424-599-197424
Sequence 197424, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 24.6'
Matches 48; Conservative
                                                   41; Conservative
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ORGANISM: Glycine max
                              Similarity
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### APPLICANITY AND, HIS TOTAL CESSENTIAL Genes in Microorganisms | TITLE OF INVENTION: Identification of Essential Genes in Microorganisms | FILE REFERENCE: ELITRA.034A |
CURRENT APPLICATION NUMBER: US/10/282,122A |
CURRENT FILING DATE: 2003-02-20 |
PRIOR APPLICATION NUMBER: 60/201,078 |
PRIOR FILING DATE: 2000-03-21 |
PRIOR PELICATION NUMBER: 60/200,727 |
PRIOR FILING DATE: 2000-05-26 |
PRIOR PELICATION NUMBER: 60/230,335 |
PRIOR FILING DATE: 2000-09-06 |
PRIOR FILING DATE: 2000-09-06 |
PRIOR PELICATION NUMBER: 60/242,578 |
PRIOR PELICATION NUMBER: 60/242,578 |
PRIOR PELICATION NUMBER: 60/253,625 |
PRIOR PELICATION NUMBER: 60/253,625 |
PRIOR PELICATION NUMBER: 60/253,625 |
PRIOR PELICATION NUMBER: 60/257,931 |
PRIOR PELICATION NUMBER: 60/269,308 |
PRIOR PELING DATE: 2000-12-22 |
PRIOR PELING DATE: 2000-12-22 |
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-----GKEGVITVEEGTGLBDELDVVEGMQFDRGYLSPYFINK 207
                                                                                                                                                                      208 PEAGSIELENPYILLVDKKISNIRELLPVLEGVAKASKPLVIIAEDVEGEALATL---- 262
                                                                                                                           -----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
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                                                                                                                                                                                                                                                                              72 AMRNIBARGLKOMKRQGDANVKGEBGIVKAHLLIGVHDD---IVSMEYDLAY-----
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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7.5%; Score 80.5; D
Best Local Similarity 18.1%; Pred. No. 22;
Matches 43; Conservative 43; Mismatches
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
Trawick, John
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TS-10-282-122A-56251
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                     APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
File Reperence: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 324
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 TSNHHHQQGNNNRVPDDPYAKVKFKIPSFWGYYDAEKYLNXEMTVEQKFSAHLVPKQHRV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 VLETQEPSKEEVSSSNDSGHPKDTVYDSSG-----NIDAQATRQARLRHHLRTNRTGMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFLLIAAVAFV-AVSADPIHYDKITEEINKAIDDAIAAI---EQSETID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Clone ID: PAT_MRT4530_64965C.1.pep
US-10-437-963-166236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.5%; Score 80.5; DB 16;
Best Local Similarity 20.3%; Pred. No. 11;
Matches 43; Conservative 34; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
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                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(324)
FOTHER INFORMATION: unsure at all Xaa locations
FOTHER EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 THVISDIODFVVALSLEISDEGNITMTSFEVR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 RQASSEFKDFAIMWXTGLADEGVLPTTWEELK 303
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18.6%; Pred. No. 22;
tive 42; Mismatches
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Barbazuk, Brad
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
Matches 44; Conserv
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Sequence 10217, Application US/10369493

Sequence 10217, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Black, Gregory J.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 FANVVNH-----IGGLS-----ILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAF 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                            102 HLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQ
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                                                                        7.5%; Score 80; DB 16; Length 600; 25.1%; Pred. No. 29; Ive 24; Mismatches 74; Indels
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// Sequence 5468, Application US/09738626

// Publication No. US20020197605A1

// GENERAL INFORMATION:

// APPLICANT: NAKAGAWA, SATOSHI

// APPLICANT: MISCOGUCH! HIROSHI

// APPLICANT: HAYSHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10217
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                                                                                                                                                                             Conservative
                                                                                                                   Best Local Similarity
Matches 45; Conserv
US-10-437-963-144132
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US-10-369-493-10217
                                                                                 Query Match
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; Sequence 144122, Application US/10437963
; Publication No. US2004012334341
; Publication No. US2004012334341
; Publication No. US2004012334341
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bucharov, Andrey A.
; APPLICANT: Brabauk, Brad
; APPLICANT: Brabauk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION UNMERR: US/10/437,963
; CURRENT APPLICATION UNMERR: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Go., Yorgwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Go., Yorgwei
APPLICANT: Go., Yorgwei
APPLICANT: Go., Yorgwei
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5.2052)B
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5550
LENGTH: 160
                                                                                                                                                                             208 PETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLVIIAEDVEGBALATL---- 262
----GKEGVITVEDGTGLEDELDVVEGMQFDRGYLSPYFINK 207
                                                                                      ----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 DHADKFERHVGIVDFKGELAMR-------NIEARGLKOMKRQGDANVKGE---- 95
                                                                                                                                                                                                                                                                   160 ROFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                             263 -----VVNTWRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEEIGMELEK 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-5550
Sequence 5550, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Caenorhabditis elegans
US-10-369-493-5550
157 TVGKLIAEAMDKV---
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US-10-437-963-144132
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183 ----SDVLTAIFQDTVRKEMTKVLAPA-FKR 208
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CORGANISM: Homo sapiens
US-10-093-463-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 ELVVFKVPAK-----NSASARGDIFSEVGDVLSGAADLEDVVDFEV-IATFLEVLNE 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Indels
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; Pred. No. 46;
31; Mismatches
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PACENTIN VET: 3.0
SEQ ID NO 5468
LENGTH: 831
                                                     APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5468
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Burgess, Catherine
Liu, Xiaohong
Spytek, Kimberly
Gorman, Linda
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Tchernev, Velizar
Gangolli, Esha
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Voss, Edward
Malyankar, Uriel
Anderson, David
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
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Best Local Similarity
Matches 43; Conserv
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APPLICANT: Miles, Charles
APPLICANT: Miles, Charles
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APPLICANT: Miles, Charles
APPLICANT: Miles, Charles
APPLICANT: Tanger, Esayond 7. Jr.
TILLS OF INVESTION: No. US20032030141 Antibodies that Bind to Antigenic Polypeptic
TILLS OF INVESTION: Encoding The Antigens, and Methods of Use.
TILLS OF INVESTION: Encoding The Antigens, and Methods of Use.
CURRENT PAPLICATION NUMBER: 1202-06-34
PRIOR PLING APPLICATION NUMBER: 1202-06-34
PRIOR PLING APPLICATION NUMBER: 1202-06-34
PRIOR PLING APPLICATION NUMBER: 1203-1203
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; Pred. No. 2.9e+02;
43; Mismatches 79; Indels 96;
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Best Local Similarity 19.9%;
Matches 54; Conservative 4:
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121 ------KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVR 160
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PRIOR FULLING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PELICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

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PRIOR FILING DATE: 2000-10-23

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PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2010-12-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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17.8%; Pred. No. 28;
Live 42; Mismatches
                                                                                                               Sequence 73215, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 17.8°
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick, John
Carr, Grant
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ROFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - See File Wrapper or PALM.
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--LAPAEFER 898
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FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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17.7%; Pred. No. 14;
tive 46; Mismatches
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                                                                                                                                                                                            Sequence 68540, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267, 636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
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ORGANISM: Proteus mirabilis
US-10-282-122A-68540
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Forsyth, R.
   Conservative
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Carr, Grant
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Best Local Similarity
Matches 42; Conserv
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Sequence 76037, Application US/10282122A
Publication No. US20040029129A1
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10-28-122A-44041
Sequence 4041, Application US/10282122A
Publication No. US20040029129A1
                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Systind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM: Salmonella typhi
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APPLICANT:
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA, 034A
CURRENT FILING DATE: 2003-02-20
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PLILNG DATE: 2000-09-06
PRIOR PLILNG DATE: 2000-09-06
PRIOR PLILNG DATE: 2000-09-06
PRIOR PPLICATION NUMBER: 60/230,335
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR PLILNG DATE: 2000-11-23
PRIOR PLILNG DATE: 2000-11-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PPLICATION NUMBER: 60/256,636
PRIOR PLILNG DATE: 2001-12-20
PRIOR PPLING DATE: 2001-10-23
PRIOR PPLING DATE: 2001-02-09
PRIOR PLILNG DATE: 2001-02-09
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 ETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATL----
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                                        Sequence 75259, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: ABSLDeck, Robert
APPLICANT: APSLICANT: Olsen, Kari
APPLICANT: Olsen, Kari
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yerryth, R.
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; ORGANISM: Salmonella typhimurium
US-10-282-122A-75259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.1
SEQ ID NO 75259
LENGTH: 548
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Best Local Similarity
Matches 42; Conserva
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RESULT 93 US-10-282-122A-76037

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73 MRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY------ 120
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                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-21
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-36
PRIOR PLING DATE: 2000-12-36
PRIOR PLING DATE: 2000-12-26
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT PILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 7.4%; Score 79.5; DE Best Local Similarity 17.8%; Pred. No. 29; Matches 42; Mismatches
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111 IVSMEYDLAYKLGDLHPTTHVIS------DIQDFVVALSLEISDEGNITMTSFEVRQ 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 LAIGGLAFAMSGGKDVEVPDVTNETKAAASQALQSAGLKVDSETKKIPD--DKIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 ---EGKVVKTDPEAKSSVKKDRSVTLYISSGTEKIEMADYTNESYESAVEALKKLGFSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | : | | : | 510 YTNAVNALAQL-----GISESQITRVDQASDTVEPGLVITQDPA 548
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
APPLICANT: Xu, H. Howard
TTTLE OF INVENTION: Identification of Essential Genes in
TTTLE OF INVENTION: Prokaryotes
FILE PEREMENT ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PILING DATE: 2001-03-21
PRIOR PRING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/25,931
PRIOR PLICATION NUMBER: 60/25,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
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PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PRIOR DATE: 2000-12-22
PRIOR PRIOR DATE: 2000-12-16
SEQ ID NO 10901
LENGTH: 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.4%; Score 79.5; D. Best Local Similarity 19.9%; Pred. No. 42; Matches 45; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53037, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Bssential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKV-----
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7.4%; Score 79.5; DB 12; Length 6.
Best Local Similarity 21.6%; Pred. No. 38;
Matches 35; Conservative 31; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 KROGDANVKGEEGI-----VKAHLLIGVHDDIVSMEYDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE REFERENCE: BLITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/2-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR PILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/25,931

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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                                                 Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                   . carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                               Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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LENGTH: 664
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Gaps

47;

454

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                  Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                      APPLICANT:
                                                                    APPLICANT:
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Sequence 1091, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Unith W.
APPLICANT: Yskind, Unith W.
APPLICANT: Trawick, John D.

US-09-815-242-10901

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Sequence 126, 48pplication US/10369493

Sequence 126, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Goo, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

FILE REPRENCE: 38-10 (52052) B.

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT APPLICATION NUMBER: US 60/360, 039

PRIOR APPLICATION NUMBER: US 60/360, 039

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 126

LENGTH: 1006
                                                                                                                                                                                                       65 -VDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLG 123
                                                                                                                                                                                                                                                                                                                    124 DIHPTTHVISDIQDFVVALSLEISDEG-----NITMTSFEVROFANVVNHIGGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                           227 SRNRSTSMI -- LNDILSQLRYDGSADGIKSLINATREKLSCKRFLVVIDDIASIETWNSI 284
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                                                                                                                               : : | :: | :: | :: | :: | 1.0 PCEVIIQLIMEDMEGESVQHPK---VVSIVĞFGGLGKTTLASQVYKKIHSRFECAVFVFA
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                                                                                          19 PIHYDKI-----TEBINKA----IDDAIAAIEQSBTIDPMKVPDHADKFERHVGI--
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                                       29; Gaps
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                                       Indels
                                 97;
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20.5%; Pred. No. 68;
tive 43; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 SGAFVETWNSGSRIITTTRRKDVANACCSSF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                          179 FGVLSDVLTA---IFQDTVRKEMTKVLAPAF 206
         Best Local Similarity 21.3%; Pred. No. 48;
Matches 45; Conservative 40; Mismatches
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US-10-219-834-150
Sequence 150, Application US/10219834
; Publication No. US20030096751A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Conservative
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Best Local Similarity
Matches 50; Conserv
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; Sequence 14847, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buckharov, Andrey A.
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPSPYDRLILEDVVRYVGDEVAIVAAIDEKTAIKAMNLIKV----KYEVLTPVLDFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.4%; Score 79.5; DB 12; Length 722; Best Local Similarity 23.0%; Pred. No. 42; Matches 38; Conservative 33; Mismatches 57; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SEQ ID NO 5:0784E: PatentIn version 3.1 LENTH: 722
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US-10-437-963-148847
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR PELLOATION NUMBER: 60/207,727
PRIOR PELLOATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-112-7
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PELLOG DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-148847
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                                                                                                                                                                                                      53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1615;
                                                                                                                               Query Match
7.4%; Score 79.5; DB 14; Length:
Best Local Similarity 20.9%; Pred. No. 1.3e+02;
Matches 41; Conservative 32; Mismatches 70; Indels
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Job time : 49 secs
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428 LGAINVTYTTVPGMLS 443
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-149
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              TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLECTIDES AND METHODS OF USE THE FILE REFERENCE: DO191 NP

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLECTIDES AND METHODS OF USE THE FILE REFERENCE: DO191 NP

CURRENT APPLICATION NUMBER: US/10/219,834

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/313,658

PRIOR FILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-09-12

PRIOR PRILING DATE: 2002-02-06

PRIOR PRILING DATE: 2002-02-06

PRIOR PRILING DATE: 2001-11-26

PRIOR PILING DATE: 2001-12-06

PRIOR FILING DATE: 2001-12-06

PRIOR PILING DATE: 2001-12-06

PRIOR PILING DATE: 2001-12-06

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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE FILE REFERENCE: DO191 NP

CURRENT APPLICATION NUMBER: US/10/219,834

CURRENT PILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/313,658

PRIOR FILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-09-12

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PRIOR PILING DATE: 2001-09-12

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PRIOR PILING DATE: 2001-12-06

PRIOR PILING DATE: 2001-12-06

PRIOR PILING DATE: 2001-12-06

PRIOR PILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 192

SOFTWARE: PatentIn version 3.1

SEQ ID NO 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| :| :| :| :| :| :| 225 TVRVNILANDNVAGIVSFQTASRSVIGHEGEILQFHVIRTFPGRGNVTVNWKIIGQNLEL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 RGLKQMKRQGDANVKGE----EGIVKAHLLIGVHDDIVSME-----YDLAYKLGDLH 126
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20.9%; Pred. No. 1.38+02;
tive 32; Mismatches 70; Indels
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Publication No. US20030096751A1
GENERAL INFORMATION:
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390 LGAINVTYTTVPGMLS 405
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Best Local Similarity 20.9%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-834-150
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